

GAATTCGGAG GAATTATTCA AAACATAAAC ACAATAAACA ATTTGAGTAG TTGCCGCACA	60
CACACACAGA CACAGCCCGT GGATTATTAC ACTAAAAGCG ACACTCAATC CAAAAAATCA	120
GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA	171
Met His Trp Ile Lys Cys Leu Leu Thr Ala	
1 5 10	
TTC ATT TGC TTC ACA GTC ATC GTG CAG GTT CAC AGT TCC GGC AGC TTT	219
Phe Ile Cys Phe Thr Val Ile Val Gln Val His Ser Ser Gly Ser Phe	
15 20 25	
GAG TTG CGC CTG AAG TAC TTC AGC AAC GAT CAC GGG CGG GAC AAC GAG	267
Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asp His Gly Arg Asp Asn Glu	
30 35 40	
GGT CGC TGC TGC AGC GGG GAG TCG GAC GGA GCG ACG GGC AAG TGC CTG	315
Gly Arg Cys Cys Ser Gly Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu	
45 50 55	
GGC AGC TGC AAG ACG CGG TTT CGC GTC TGC CTA AAG CAC TAC CAG GCC	363
Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Gln Ala	
60 65 70	
ACC ATC GAC ACC ACC TCC CAG TGC ACC TAC GGG GAC GTG ATC ACG CCC	411
Thr Ile Asp Thr Thr Ser Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro	
75 80 85 90	
ATT CTC GGC GAG AAC TCG GTC AAT CTG ACC GAC GCC CAG CGC TTC CAG	459
Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asp Ala Gln Arg Phe Gln	
95 100 105	
AAC AAG GGC TTC ACG AAT CCC ATC CAG TTC CCC TTC TCG TTC TCA TGG	507
Asn Lys Gly Phe Thr Asn Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp	
110 115 120	

FIG.1A

CCG GGT ACC TTC TCG CTG ATC GTC GAG GCC TGG CAT GAT ACG AAC AAT	555
Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asp Thr Asn Asn	
125 130 135	
AGC GGC AAT GCG CGA ACC AAC AAG CTC CTC ATC CAG CGA CTC TTG GTG	603
Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Gln Arg Leu Leu Val	
140 145 150	
CAG CAG GTA CTG GAG GTG TCC TCC GAA TGG AAG ACG AAC AAG TCG GAA	651
Gln Gln Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu	
155 160 165 170	
TCG CAG TAC ACG TCG CTG GAG TAC GAT TTC CGT GTC ACC TGC GAT CTC	699
Ser Gln Tyr Thr Ser Leu Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu	
175 180 185	
AAC TAC TAC GGA TCC GGC TGT GCC AAG TTC TGC CGG CCC CGC GAC GAT	747
Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp	
190 195 200	
TCA TTT GGA CAC TCG ACT TGC TCG GAG ACG GGC GAA ATT ATC TGT TTG	795
Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu	
205 210 215	
ACC GGA TGG CAG GGC GAT TAC TGT CAC ATA CCC AAA TGC GCC AAA GGC	843
Thr Gly Trp Gln Gly Asp Tyr Cys His Ile Pro Lys Cys Ala Lys Gly	
220 225 230	
TGT GAA CAT GGA CAT TGC GAC AAA CCC AAT CAA TGC GTT TGC CAA CTG	891
Cys Glu His Gly His Cys Asp Lys Pro Asn Gln Cys Val Cys Gln Leu	
235 240 245 250	
GGC TGG AAG GGA GCC TTG TGC AAC GAG TGC GTT CTG GAA CCG AAC TGC	939
Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys	
255 260 265	

FIG.1B

ATC CAT GGC ACC TGC AAC AAA CCC TGG ACT TGC ATC TGC AAC GAG GGT Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly 270 275 280	987
TGG GGA GGC TTG TAC TGC AAC CAG GAT CTG AAC TAC TGC ACC AAC CAC Trp Gly Gly Leu Tyr Cys Asn Gln Asp Leu Asn Tyr Cys Thr Asn His 285 290 295	1035
AGA CCC TGC AAG AAT GGC GGA ACC TGC TTC AAC ACC GGC GAG GGA TTG Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu 300 305 310	1083
TAC ACA TGC AAA TGC GCT CCA GGA TAC AGT GGT GAT GAT TGC GAA AAT Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn 315 320 325 330	1131
GAG ATC TAC TCC TGC GAT GCC GAT GTC AAT CCC TGC CAG AAT GGT GGT Glu Ile Tyr Ser Cys Asp Ala Asp Val Asn Pro Cys Gln Asn Gly Gly 335 340 345	1179
ACC TGC ATC GAT GAG CCG CAC ACA AAA ACC GGC TAC AAG TGT CAT TGC Thr Cys Ile Asp Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys 350 355 360	1227
GCC AAC GGC TGG AGC GGA AAG ATG TGC GAG GAG AAA GTG CTC ACG TGT Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys 365 370 375	1275
TGC GAC AAA CCC TGT CAT CAG GGA ATC TGC CGC AAC GTT CGT CCT GGC Ser Asp Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly 380 385 390	1323
TTG GGA AGC AAG GGT CAG GGC TAC CAG TGC GAA TGT CCC ATT GGC TAC Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr 395 400 405 410	1371

FIG.1C

AGC GGA CCC AAC TGC GAT CTC CAG CTG GAC AAC TGC AGT CCG AAT CCA Ser Gly Pro Asn Cys Asp Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro 415 420 425	1419
TGC ATA AAC GGT GGA AGC TGT CAG CCG AGC GGA AAG TGT ATT TGC CCA Cys Ile Asn Gly Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro 430 435 440	1467
GCG GGA TTT TCG GGA ACG AGA TGC GAG ACC AAC ATT GAC GAT TGT CTT Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu 445 450 455	1515
GGC CAC CAG TGC GAG AAC GGA GGC ACC TGC ATA GAT ATG GTC AAC CAA Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asp Met Val Asn Gln 460 465 470	1563
TAT CGC TGC CAA TGC GTT CCC GGT TTC CAT GGC ACC CAC TGT AGT AGC Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser 475 480 485 490	1611
AAA GTT GAC TTG TGC CTC ATC AGA CCG TGT GCC AAT GGA GGA ACC TGC Lys Val Asp Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys 495 500 505	1659
TTG AAT CTC AAC AAC GAT TAC CAG TGC ACC TGT CGT GCG GGA TTT ACT Leu Asn Leu Asn Asn Asp Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr 510 515 520	1707
GGC AAG GAT TGC TCT GTG GAC ATC GAT GAG TGC AGC AGT GGA CCC TGT Gly Lys Asp Cys Ser Val Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys 525 530 535	1755
CAT AAC GGC GGC ACT TGC ATG AAC CGC GTC AAT TCG TTC GAA TGC GTG His Asn Gly Gly Thr Cys Met Asn Arg Val Asn Ser Phe Glu Cys Val 540 545 550	1803

FIG.1D

168.37730 147

TGT GCC AAT GGT TTC AGG GGC AAG CAG TGC GAT GAG GAG TCC TAC GAT Cys Ala Asn Gly Phe Arg Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp 555 560 565 570	1851
TCG GTG ACC TTC GAT GCC CAC CAA TAT GGA GCG ACC ACA CAA GCG AGA Ser Val Thr Phe Asp Ala His Gln Tyr Gly Ala Thr Thr Gln Ala Arg 575 580 585	1899
GCC GAT GGT TTG ACC AAT GCC CAG GTA GTC CTA ATT GCT GTT TTC TCC Ala Asp Gly Leu Thr Asn Ala Gln Val Val Leu Ile Ala Val Phe Ser 590 595 600	1947
GTT GCG ATG CCT TTG GTG GCG GTT ATT GCG GCG TGC GTG GTC TTC TGC Val Ala Met Pro Leu Val Ala Val Ile Ala Ala Cys Val Val Phe Cys 605 610 615	1995
ATG AAG CGC AAG CGT AAG CGT GCT CAG GAA AAG GAC GAC GCG GAG GCC Met Lys Arg Lys Arg Lys Arg Ala Gln Glu Lys Asp Asp Ala Glu Ala 620 625 630	2043
AGG AAG CAG AAC GAA CAG AAT GCG GTG GCC ACA ATG CAT CAC AAT GGC Arg Lys Gln Asn Glu Gln Asn Ala Val Ala Thr Met His His Asn Gly 635 640 645 650	2091
AGT GGG GTG GGT GTA GCT TTG GCT TCA GCC TCT CTG GGC GGC AAA ACT Ser Gly Val Gly Val Ala Leu Ala Ser Ala Ser Leu Gly Gly Lys Thr 655 660 665	2139
GGC AGC AAC AGC GGT CTC ACC TTC GAT GGC GGC AAC CCG AAT ATC ATC Gly Ser Asn Ser Gly Leu Thr Phe Asp Gly Gly Asn Pro Asn Ile Ile 670 675 680	2187
AAA AAC ACC TGG GAC AAG TCG GTC AAC AAC ATT TGT GCC TCA GCA GCA Lys Asn Thr Trp Asp Lys Ser Val Asn Asn Ile Cys Ala Ser Ala Ala 685 690 695	2235

FIG.1E

GCA GCG GCG GCG GCG GCA GCA GCG GCG GAC GAG TGT CTC ATG TAC GGC Ala Ala Ala Ala Ala Ala Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly 700 705 710	2283
GGA TAT GTG GCC TCG GTG GCG GAT AAC AAC AAT GCC AAC TCA GAC TTT Gly Tyr Val Ala Ser Val Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe 715 720 725 730	2331
TGT GTG GCT CCG CTA CAA AGA GCC AAG TCG CAA AAG CAA CTC AAC ACC Cys Val Ala Pro Leu Gln Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr 735 740 745	2379
GAT CCC ACG CTC ATG CAC CGC GGT TCG CCG GCA GGC AGC TCA GCC AAG Asp Pro Thr Leu Met His Arg Gly Ser Pro Ala Gly Ser Ser Ala Lys 750 755 760	2427
GGA GCG TCT GGC GGA GGA CCG GGA GCG GCG GAG GGC AAG AGG ATC TCT Gly Ala Ser Gly Gly Gly Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser 765 770 775	2475
GTT TTA GGC GAG GGT TCC TAC TGT AGC CAG CGT TGG CCC TCG TTG GCG Val Leu Gly Glu Gly Ser Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala 780 785 790	2523
GCG GCG GGA GTG GCC GGA GCC TGT TCA TCC CAG CTA ATG GCT GCA GCT Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Gln Leu Met Ala Ala Ala 795 800 805 810	2571
TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG CGA TCC GTG Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val 815 820 825	2619
GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT Val Cys Gly Thr Pro His Met 830	2670
AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGGTT GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTGTGTTG ATTGAAGCAG TTAGTCGTC ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC	2730 2790 2850 2892

FIG.1F

	SP	EGF	N	TM	cdc10	PA	opo	% AGGREGATION WITH DI	WITH Ser
1.pMINMg								40	21
2.ΔSph	1		32					0	nt
3.ΔClo	7		31					0	nt
4.ΔEGF(7-17)	7	17						0	nt
5.ΔEGF(9-26)	9	26						0	nt
6.ΔEGF(17-30)	17	31						22	nt
7.ΔEGF(7-9)	7 9							20	14
8.ΔEGF(9-17)	9	17						0	0
9.ΔEGF(17-26)	17	26						10	8
10.ΔEGF(26-30)	26	31						5	7
11.ΔEGF(9-30)	9	31						0	nt
12.ΔEGF(7-26)	7	26						0	nt
13.ΔClo+EGF(9-17)	7 9 17	31						35	20
14.ΔClo+EGF(17-26)	7	17 26 31						0	nt
15.SPLIT	14							42	nt
16.ΔClo+EGF(9-13)	7 9 13	31						47	25

FIG.2A

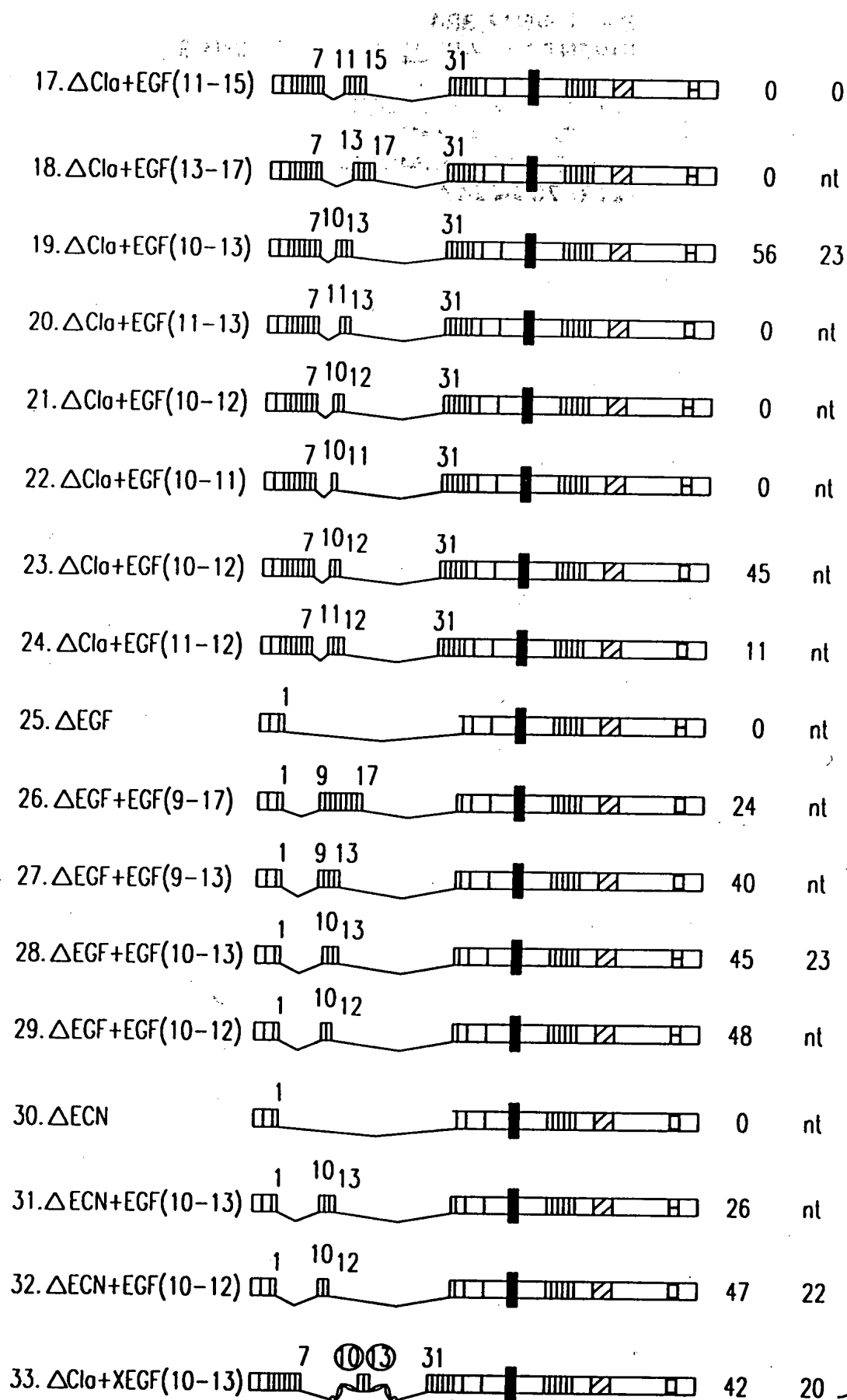


FIG.2B

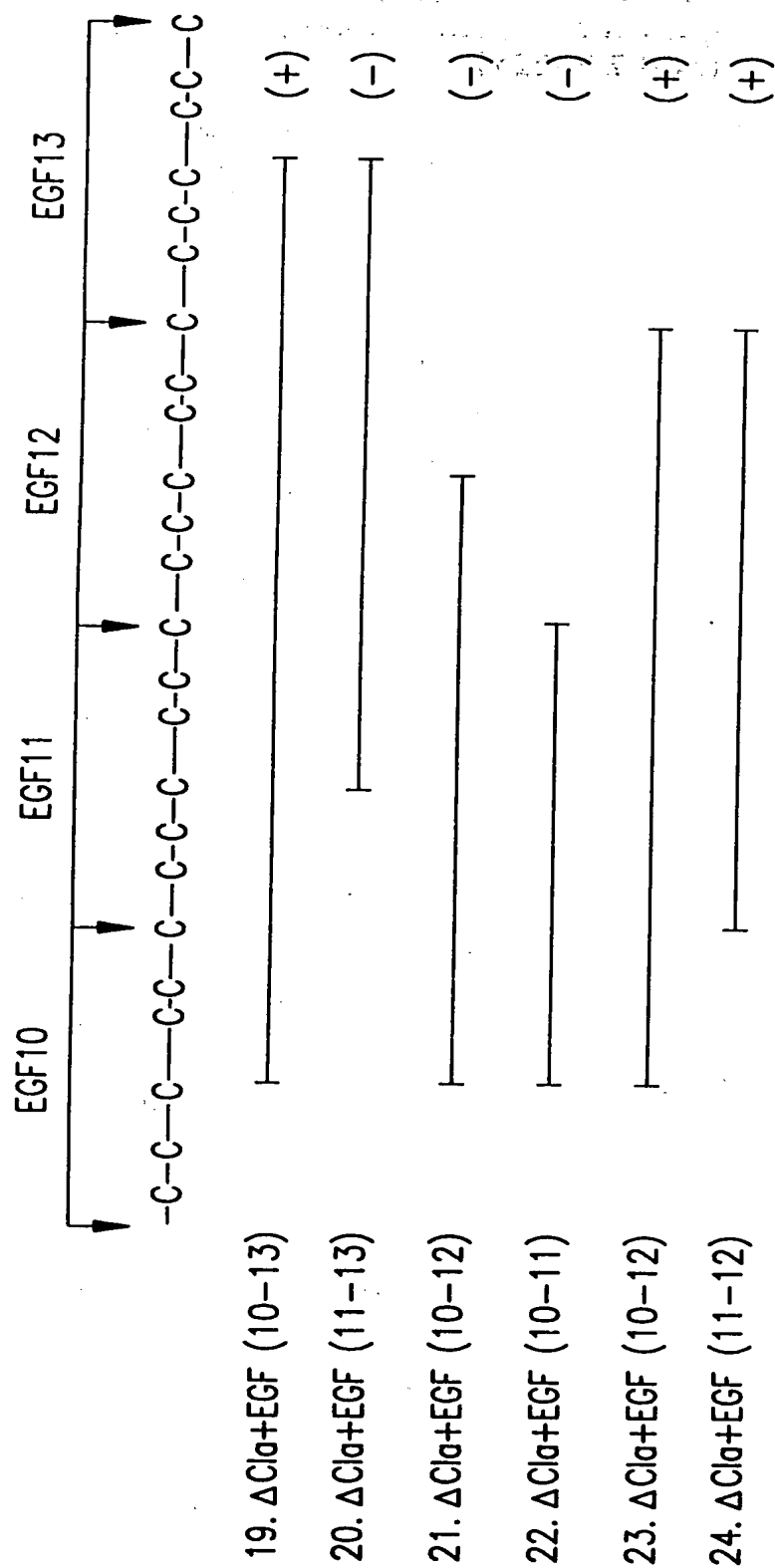


FIG.3

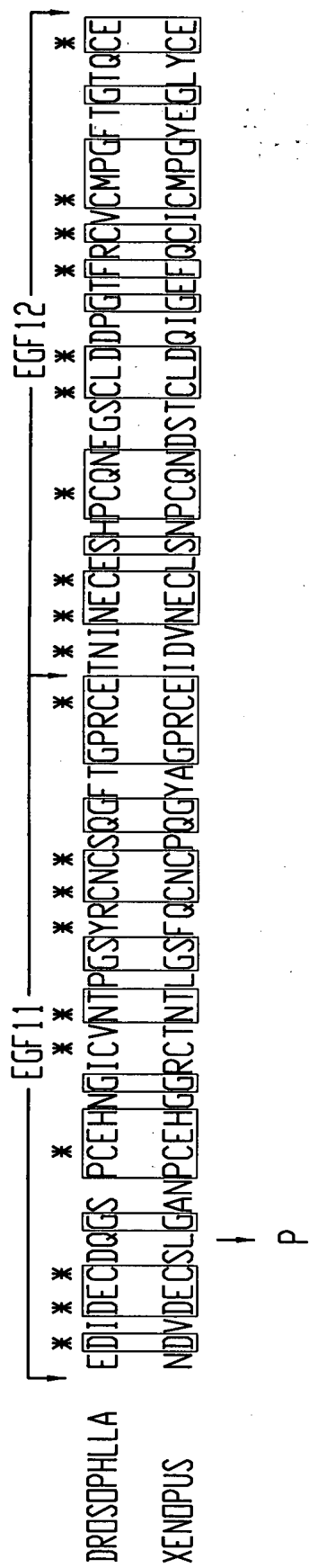


FIG.4

1 CCGAGTCGAGCGCGGTGCTTCGAGCGGTGATGAGCCCTTTCTGTCAACGCTAAAGATC
 121 AAGCACATACTAAGGTCCATATAATAATAATAATTTGTGTGATACAAACATTAT
 241 GGGCGTTATTCAGCTATCCAGAGCAAGTGTAGTGGCAAAATAGAAACAAACAAAGGCA
 361 CAATCCAGAGTGAATCCGAAACAACTCCATCTAGATCGCCAACCAAGCATCACGCTCGCA

 481 TCGTCGTTGGAGTCAACAATAGAAATCAGCAGACGCTGGGAATGTCCAAGAGACGGCG
 SerSerLeuGluSerThrIleGluSerAlaAspSerLeuGlyMetSerLysLysThrAla

 601 CGCGATTGTCGATCATTAAGTCTGCCCTGCAACTTAATTGCTTTAATTTAATACTGTTA
 ArgAspCysArgSerLeuLysSerAlaCysAsnLeuIleAlaLeuIleLeuLeu

 721 AACAGCCATCTACTCAACGGCTATTGCTGGCGCATGCCAGCGGAACCTAGGGCCACCAG
 AsnSerHisLeuLeuAsnGlyTyrCysCysGlyMetProAlaGluLeuArgAlaThrLys

 841 ACCGAGCAGGGTGCCAGCATATCCACGGGTGTTGCTTTGGCAACGCCACCACCAAGATA
 ThrGluGlnGlyAlaSerIleSerThrGlyCysSerPheGlyAsnAlaThrThrLysIle
 #2
 961 ACGTTTCGTTGGACGAAGTCGTTACGCTGATACTGCAGGCGTTGGATATGTACACACA
 ThrPheArgTrpThrLysSerPheThrLeuIleLeuGlnAlaLeuAspMetTyrAsnThr
 #3
 1081 TCGCCGGAGTGAAGACGCTGGACCACATCGGGCGGAACGGCGGATCACCTACCGTGTC
 SerProGluTrpLysThrLeuAspHisIleGlyArgAsnAlaArgIleThrTyrArgVal

 1201 GACGATCAGTTCGGTCACTACGCCCTGGGCTCCGAGGGTCAGAGCTCTGCCTGAATGGC
 AspAspGlnPheGlyHisTyrAlaCysGlySerGluGlyGlnLysLeuCysLeuAsnGly

FIG. 5A

TACAAACATCAGCGCCTATCAAGTGGAGTGTCAGTGTAACAAACAAACGAGAG
CCAAACAAAACCAACAAACGAGGAAAGTGGAGAAAATGATACAGCATCCAGAGTAC
CCAAAATCTGCATACATGGGCTAATTAAAGGCTGCCAGCGAATTTACATTTGTGTGTC
ACGCCCCCAGAAATGTACAAAATGTTTAGGAACATTTTCGGCGAAACACGACTACGTCG
MetPheArgLysHisPheArgArgLysProAlaThrSer 13
ACAAAAGGCAGGTCGGAGGCATCGGGTACCCAAAATCGCGACCTGCCATCGACGATC
ThrLysArgGlnArgProArgHisArgValProLysIleAlaThrLeuProSerThrIle 53
GTCCATAAGATATCCGCAGCTGGTAACCTCGAGCTGGAAATATTAGAAATCTCAAAATACC
ValHisLysIleSerAlaAlaGlyAsnPheGluLeuGluIleLeuGluIleSerAsnThr 93
-----#1
ACGATAGGCTGCTCGCCATGCACGACGGCATTTCCGGCTGTCCTGAAGGAGTACCAGACC
ThrIleGlyCysSerProCysThrThrAlaPheArgLeuCysLeuLysGluTyrGlnThr 133
CTGGGTGGCTCCAGCTTTGTGCTCAGCGATCCGGGTGTGGGAGCCATTGTGCTGCCCTTT
LeuGlyGlySerSerPheValLeuSerAspProGlyValGlyAlaIleValLeuProPhe 173
TCCTATCCAGATCGGGAGAGGTTAATTGAGGAACATCATCTCGGGGTGATGCTGCCG
SerTyrProAspAlaGluArgLeuIleGluGluThrSerTyrSerGlyValIleLeuPro 213
#4
CGGGTGCAATGGCGCGTTACCTACTACACACGACCTGCACGACCTTGTCCGTCGCGGG
ArgValGlnCysAlaValThrTyrTyrAsnThrThrCysThrThrPheCysArgProArg 253
TGGCAGGGCGTCAACTGCGAGGAGGCCATATGCAAGGGGGGTGCGACCCCGTCCACGGC
TrpGlnGlyValAsnCysGluGluAlaIleCysLysAlaGlyCysAspProValHisGly 293

FIG.5B

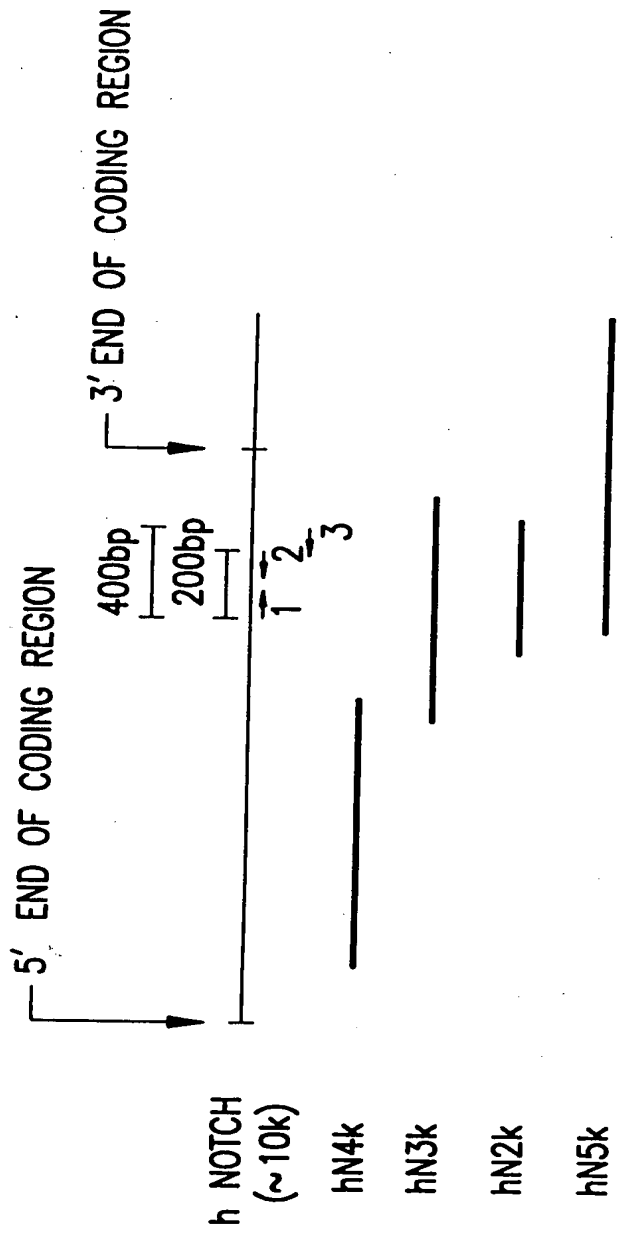


FIG.6

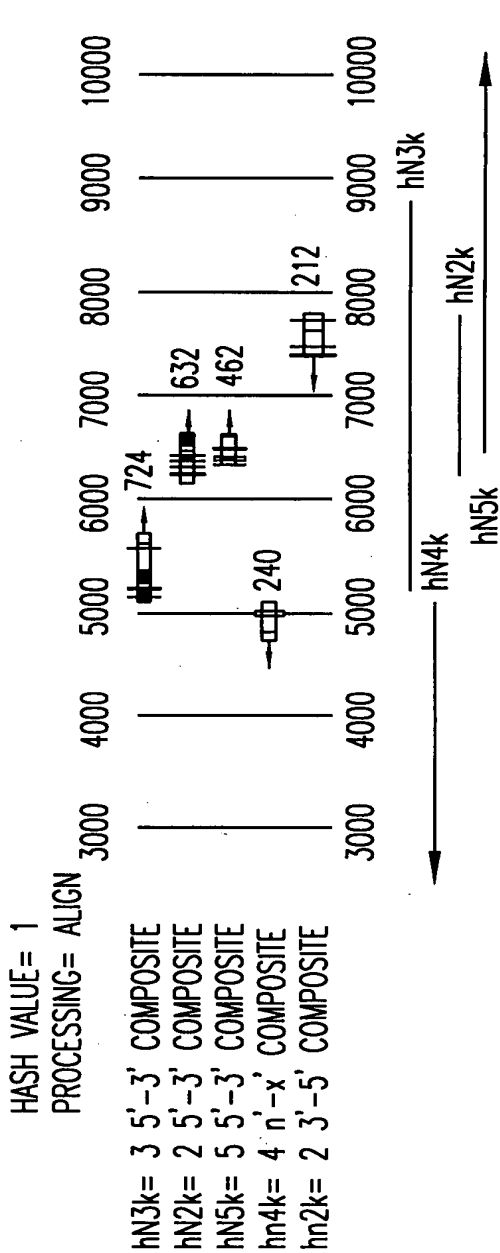
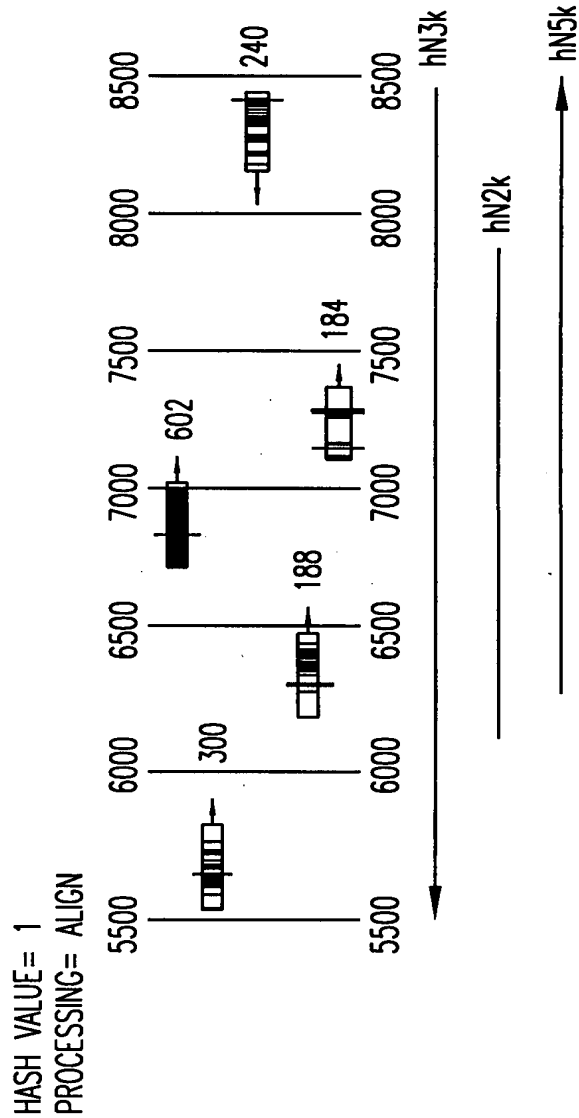


FIG. 7



1 GAATTCGCT GGGAGAATGG TCTGAGCTAC CTGCCCCTCC TGCTGGGGCA TCAATGGCAA
 61 GTGGGGAAAG CCACACTGGG CAAACGGGCC AGGCCATTTC TGGAAATGTTG TACATGGTGG
 121 GCAGGGGGCC CGCAACAGCT GGAGGGCAGG TGGACTGAGG CTGGGGATCC CCCGCTGGTT
 181 GGGCAATACT GCCTTTACCC ATGAGCTGGA AAGTCACAAT GGGGGGCAAG GGCTCCCGAG
 241 GGTGGTTATG TGCTTCCTTC AGGTGGC

FIG.8A

1 GAATTCCTTC CATTATACGT GACTTTTCTG AACTGTAGC CACCCTAGTG TCTCTAACTC
 61 CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GCTCCTTAAT
 121 GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC
 181 AACCCGGAAC TGAAGGCTGG CTCTCACCT CTAGGCAGAG CAGGAATTCC GAGGTGGATG
 241 TGTTAGATGT GAATGTCCGT GGCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCTCC
 301 GAGGAGGCAG CTCAGATTTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACA
 361 TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGAC CAGACAGACC GGACTGGTGA
 421 GATGGCCCTG CACCTTGAG CCCGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA
 481 TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCCGC TGTCCACTCC ATGCTGCAGT
 541 GGCACGTGAT GCCAAGGTGT ATTCAGATCT GTTA

FIG.8B

1 TCCAGATTCT GATTCGCAAC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA
 61 CACCCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT
 121 GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTAC TGGGCAGCTG
 181 CTGTCAATAA TGTGGAGGCA ACTCTTTTGT TGTGAAAAA TGGGGCCAAC CGAGACATGC
 241 AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCC GGAGGAGCTA TAAGC

FIG.8C

1 GAATTCATT CAGGAGGAAA GGGTGGGGAG AGAAGCAGGC ACCCACTTTC CCGTGGCTGG
61 ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CGGAGTGCCA
121 TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA
181 GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG
241 CAGAGCTG

FIG.9A

1 CTAAAGGGAA CAAAAGCNGG AGCTCCACCG CGGGCGGCNC NGCTCTAGAA CTAGTGGANN
61 NCCCGGGCTG CAGGAATTCC GCGGACTGG GTCGGGCTC AGAGCGGGCG TGTGGAAGAG
121 ATTCTAGACC GGGAGAACAA GCGAATGGCT GACAGCTGGC CTCCAAAGTC ACCAGGCTCA
181 AATCGCTCGC CCTGGACATC GAGGGATGCA GAGGATCAGA ACCGGTACCT GGATGGCATG
241 ACTCGGATTT ACAAGCATGA CCAGCCTGCT TACAGGGAGC GTGANNTTTT CACATGCAGT
301 CGACAGACAC GAGCTCTATG CAT

FIG.9B

10 20 30 40
 * * * *
 TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC
 C Q E D A G N K V C S L Q C N N>
 50 60 70 80 90
 * * * *
 CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC
 H A C G G W D G G D C S L N F N D>
 100 110 120 130 140
 * * * *
 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT
 P W K N C T Q S L Q C W K Y F S>
 150 160 170 180 190
 * * * *
 GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC
 D G H C C D S Q C C N S A G C L F D>

FIG. 10A

200 210 220 230 240
 * * * * *
 GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC
 G F D C Q R A E G Q C N P L Y D> -

 250 260 270 280
 * * * * *
 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC
 Q Y C K D H F S D G H C D Q G C>

 290 300 310 320 330
 * * * * *
 AAC AGC GCG GAG TGC GAG TGG GAC GGC CTG GAC TGT GCG GAG CAT GTA
 N S A E C E W D G L D C A E H V>

 340 350 360 370 380
 * * * * *
 CCC GAG AGG CTG GCG GCC GGC ACG CTG GTG GTG GTG CTG ATG CCG
 P E R L A A G T L V V V L M P>

FIG.10B

390	400	410	420	430
* CCG GAG CAG CTG CGC AAC AGC TCC TTC CAC TTC CTG CGG GAG CTC AGC	* * * * *	* * * * *	* * * * *	* * * * *
P E Q L R N S S F H F L R E L S>				
440	450	460	470	480
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
CGC GTG CTG CAC ACC AAC GTG GTC TTC AAG CGT GAC GCA CAC GGC CAG				
R V L H T N V V F K R D A H G Q>				
490	500	510	520	
* * * * *	* * * * *	* * * * *	* * * * *	
CAG ATG ATC TTC CCC TAC TAC GGC CGC GAG GAG GAG CTG CGC AAG CAC				
Q M I F P Y Y G R E E L R K H>				
530	540	550	560	570
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
CCC ATC AAG CGT GCC GCC GAG GGC TGG GCC GCA CCT GAC GCC CTG CTG				
P I K R A A E G W A A P D A L L>				

FIG. 10C

580 * * * * * 590 600 610 620
 GGC CAG GTG AAG GCC TCG CTG CTC CCT GGT GGC AGC GAG GGT GGG CCG
 G Q V K A S L L P G G S E G G R>

 630 640 650 660 670
 * * * * *
 CCG CGG AGG GAG CTG GAC CCC ATG GAC GTC CGC GGC TCC ATC GTC TAC
 R R E L D P M D V R G S I V Y>

 680 690 700 710 720
 * * * * *
 CTG GAG ATT GAC AAC CCG CAG TGT GTG CAG GCC TCC TCG CAG TGC TTC
 L E I D N R Q C V Q A S S Q C F>

 730 740 750 760
 * * * * *
 CAG AGT GCC ACC GAC GTG GCC GCA TTC CTG GGA GGC CTC GCC TCG CTG
 Q S A T D V A A F L L G A L A S L>

FIG. 10D

770	*		780		790		800		810	
	*		*	*	*	*	*	*	*	*
GGC	AGC	CTC	AAC	ATC	CCC	TAC	AAG	ATC	GAG	GCC
G	S	L	N	I	P	Y	K	I	E	A
										V
										Q
										S
										E
										T>
										-
820	*		830	*		840	*		850	*
	*		*	*	*	*	*	*	*	*
GTG	GAG	CCG	CCC	CCG	CCG	CAG	CTG	CAC	TTC	ATG
V	E	P	P	P	P	A	Q	L	H	F
										M
										Y
										V
										A
										A>
870	*		880	*		890	*		900	*
	*		*	*	*	*	*	*	*	*
GCC	GCC	TTT	GTG	CTT	CTG	TTC	TTC	GTG	GGC	TGC
A	A	F	V	L	L	F	F	V	G	C
										G
										V
										L
										L
										S>
920	*		930	*		940	*		950	*
	*		*	*	*	*	*	*	*	*
CGC	AAG	CGC	CGG	CGG	CAG	CAT	GGC	CAG	CTC	TGG
R	K	R	R	R	Q	H	G	Q	L	W
										F
										P
										E
										G
										F>
										TTC
										GGC
										AGT
										GAG
										ACC

FIG.10E

	970	980	990	1000
	* *	* *	* *	
AAA GTG TCT GAG GCC AGC AAG AAG AAG CGG CGG GAG CCC CTC GGC GAG				
K V S E A S K K K R R E P L G E>				
1010	1020	1030	1040	1050
* *	* *	* *	* *	
GAC TCC GTG GGC CTC AAG CCC CTG AAG AAC GCT TCA GAC GGT GCC CTC				
D S V G L K P L K N A S D G A L>				
1060	1070	1080	1090	1100
* *	* *	* *	* *	
ATG GAC GAC AAC CAG AAT GAG TGG GGG GAC GAG GAC CTG GAG ACC AAG				
M D D N Q N E W G D E D L E T K>				
1110	1120	1130	1140	1150
* *	* *	* *	* *	
AAG TTC CGG TTC GAG GAG CCC GTG GTT CTG CCT GAC CTG GAC GAC CAG				
K F R F E E P V V L P D L D D Q>				

FIG.10F

1160	1170	1180	1190	1200
* * *	* *	* *	* *	* *
ACA GAC CAC CGG CAG TGG ACT CAG CAC CTG GAT GCC GCT GAC CTG				
T D H R Q W T Q Q H L D A A D L>				
1210	1220	1230	1240	
* *	* *	* *	* *	
CGC ATG TCT GCC ATG GCC CCC ACA CCG CCC CAG GGT GAG GTT GAC GCC				
R M S A M A P T P P Q G E V D A>				
1250	1260	1270	1280	1290
* *	* *	* *	* *	* *
GAC TGC ATG GAC GTC AAT GTC CGC GGG CCT GAT GGC TTC ACC CCG CTC				
D C M D V N V R G P D G F T P L>				
1300	1310	1320	1330	1340
* *	* *	* *	* *	* *
ATG ATC GCC TCC TGC AGC GGG GGC GGC CTG GAG ACG GGC AAC AGC GAG				
M I A S C S G G G L E T G N S E>				

FIG.10G

1350 1360 1370 1380 1390
 * * * * *
 GAA GAG GAG GAC GCG CCG GCC GTC ATC TCC GAC TTC ATC TAC CAG GGC
 E E D A P A V I S D F I Y Q G>

 1400 1410 1420 1430 1440
 * * * * *
 GCC AGC CTG CAC AAC CAG ACA GAC CGC ACG GGC GAG ACC GCC TTG CAC
 A S L H N Q T D R T G E T A L HD

 1450 1460 1470 1480
 * * * *
 CTG GCC GCC CGC TAC TCA CGC TCT GAT GCC GCC AAG CGC CTG CTG GAG
 L A A R Y S R S D A A K R L L E>

 1490 1500 1510 1520 1530
 * * * * *
 GCC AGC GCA GAT GCC AAC ATC CAG GAC AAC ATG GGC CGC ACC CCG CTG
 A S A D A N I Q D N M G R T P LD

FIG.10H

1540 1550 1560 1570 1580
 * * * * *
 CAT GCG GCT GTG TCT GCC GAC GCA CAA GGT GTC TTC CAG ATC CTG ATC
 H A A V S A D A Q G V F Q I L I>

 1590 1600 1610 1620 1630
 * * * * *
 CGG AAC CGA GCC ACA GAC CTG GAT GCC CGC ATG CAT GAT GGC ACG ACG
 R N R A T D L D A R M H D G T T>

 1640 1650 1660 1670 1680
 * * * * *
 CCA CTG ATC CTG GCT GCC CGC CTG GCC GTG GAG GGC ATG CTG GAG GAC
 P L I L A A R L A V E G M L E D>

 1690 1700 1710 1720
 * * * * *
 CTC ATC AAC TCA CAC GCC GAC GTC AAC GCC GTA GAT GAC CTG GGC AAG
 L I N S H A D V N A V D D L G K>

 1730 1740 1750 1760 1770
 * * * * *
 TCC GCC CTG CAC TGG GCC GCC GCG GTG AAC AAT GTG GAT GCC GCA GTT
 S A L H W A A A V N N V D A A V>

FIG. 10I

1780	1790	1800	1810	1820
* GTG CTC CTG AAG AAC GGG GCT AAC AAA GAT ATG CAG AAC AAC AGG GAG	* * * * *	* * * * *	* * * * *	* * * * *
V L L K N G A N K D M Q N R E>				

1830	1840	1850	1860	1870
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
GAG ACA CCC CTG TTT CTG GCC GCC CGG GAG GGC AGC TAC GAG ACC GCC				
E T P L F L A A R E G S Y E T A>				

1880	1890	1900	1910	1920
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
AAG GTG CTG CTG GAC CAC TTT GCC AAC CGG GAC ATC ACG GAT CAT ATG				
K V L L D H F A N R D I T D H M>				

1930	1940	1950	1960
* * * * *	* * * * *	* * * * *	* * * * *
GAC CGC CTG CCG CGC GAC ATC GCA CAG GAG CGC ATG CAT CAC GAC ATC			
D R L P R D I A Q E R M H D I>			

FIG.10J

1970	1980	1990	2000	2010
* GTG AGG CTG CTG GAC GAG TAC AAC CTG GTG CGC AGC CCG CAG CTG CAC V R L L D E Y N L V R S P Q L HD	* 1980	* 1990	* 2000	* 2010
2020	2030	2040	2050	2060
* GGA GCC CCG CTG GGG GGC AGC CCC ACC CTG TCG CCC CCG CTC TGC TCG G A P L G G T P T L S P L C S>	* 2030	* 2040	* 2050	* 2060
2070	2080	2090	2100	2110
* CCC AAC GGC TAC CTG GGC AGC CTC AAG CCC GGC GTG CAG GGC AAG AAG P N G Y L G S L K P G V Q G K K>	* 2080	* 2090	* 2100	* 2110
2120	2130	2140	2150	2160
* GTC CGC AAG CCC AGC AGC AAA GGC CTG GCC TGT GGA AGC AAG GAG GCC V R K P S S K G G L A C G S K E A>	* 2130	* 2140	* 2150	* 2160

FIG. 10K

2170	2180	2190	2200
* * *	* * *	* * *	* * *
AAG GAC CTC AAG GCA CGG AGG AAG AAG TCC CAG GAT GGC AAG GGC TGC			
K D L K A R R K K S Q D G K G C>			
2210	2220	2230	2240
* * *	* * *	* * *	* * *
CTG CTG GAC AGC TCC GGC ATG CTC TCG CCC GTG GAC TCC CTG GAG TCA			
L L D S S G M L S P V D S L E S>			
2260	2270	2280	2290
* * *	* * *	* * *	* * *
CCC CAT GGC TAC CTG TCA GAC GTG GCC TCG CCG CCA CTG CTG CCC TCC			
P H G Y L S D V A S P P L L P S>			
2310	2320	2330	2340
* * *	* * *	* * *	* * *
CCG TTC CAG CAG TCT CCG TCC GTG CCC CTC AAC CAC CTG CCT GGG ATG			
P F Q Q S P S V P L N H L P G M>			

FIG.10L

2360 2370 2380 2390 2400
 * * * * *
 CCC GAC ACC CAC CTG GGC ATC GGG CAC CTG AAC GTG GCG GCC AAG CCC
 P D T H L G I G H L N V A A K P>

 2410 2420 2430 2440
 * * * *
 GAG ATG GCG GCG CTG GGT GGG GGC GGC CTG GCG TTT GAG ACT GGC
 E M A A L G G G G G R L A F E T G>

 2450 2460 2470 2480 2490
 * * * * *
 CCA CCT CGT CTC TCC CAC CTG CCT GTG GCG TCT GCG ACC AGC ACC GTC
 P P R L S H L P V A S G T S T V>

 2500 2510 2520 2530 2540
 * * * * *
 CTG GGC TCC AGC AGC GGA GGG GCC CTG AAT TTC ACT GTG GCG GGG TCC
 L G S S S G G A L N F T V G G S>

FIG.10M

2550 2560 2570 2580 2590
 * * * * *
 ACC AGT TTG AAT GGT CAA TGC GAG TGG CTG TCC CGG CTG CAG AGC GGC
 T S L N G Q C E W L S R L Q S G>

 2600 2610 2620 2630 2640
 * * * * *
 ATG GTG CCG AAC CAA TAC AAC CCT CTG CCG GGG AGT GTG GCA CCA GGC
 M V P N Q Y N P L R G S V A P G>

 2650 2660 2670 2680
 * * * *
 CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG
 P L S T Q A P S L Q H G M V G P>

 2690 2700 2710 2720 2730
 * * * * *
 CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC
 L H S S L A A S A L S Q M M S Y>

FIG. 10N

2740	2750	2760	2770	2780
* * *	* * *	* * *	* * *	* * *
CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CCT CAC CTG GTG CAG				
Q G L P S T R L A T Q P H L V Q>				
2790	2800	2810	2820	2830
* * *	* * *	* * *	* * *	* * *
ACC CAG CAG GTG CAG CCA AAC TTA CAG ATG CAG CAG AAC CTG				
T Q Q V Q P Q N L Q M Q Q N L>				
2840	2850	2860	2870	2880
* * *	* * *	* * *	* * *	* * *
CAG CCA GCA AAC ATC CAG CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA				
Q P A N I Q Q Q Q S L Q P P P>				
2890	2900	2910	2920	
* * *	* * *	* * *	* * *	
CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG				
P P Q P H L G V S S A A S G H L>				
2930	2940	2950	2960	2970
* * *	* * *	* * *	* * *	* * *
GGC CGG AGC TTC CTG AGT GGA GAG CCG AGC CAG GCA GAC GTG CAG CCA				
G R S F L S G E P S Q A D V Q P>				

FIG.100

2980	2990	3000	3010	3020
* CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC	* L G P S S L A V H T I L P Q E S>			
3030	3040	3050	3060	3070
* CTG GGC CCC AGC TCG TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC	* P A L P T S S L P S S L V P V T>			
3080	3090	3100	3110	3120
* GCA GGC CAG TTC CTG ACG CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT	* A A Q F L T L T P P S Q H S Y S P>			

FIG.10P

3130	3140	3150	3160
* * *	* * *	* * *	* * *
GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG			
V D N T P S H Q L Q V P V P V M>			
3170	3180	3190	3200
* * *	* * *	* * *	* * *
GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA ATT TTG ATC			
V M I R S S D P S K G S I L I>			
3220	3230		
* * *	* * *		
GAA GCT CCC GAC TCA TGG			
E A P D S W>			

FIG.10Q

1-12-80

G GAG GTG GAT GTG TTA GAT GTG AAT GTC CGT GGC CCA GAT GGC TGC Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys 1 5 10 15	46
ACC CCA TTG ATG TTG GCT TCT CTC CGA GGA GGC AGC TCA GAT TTG AGT Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser 20 25 50	94
GAT GAA GAT GAA GAT GCA GAG GAC TCT TCT GCT AAC ATC ATC ACA GAC Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp 35 40 45	142
TTG GTC TAC CAG GGT GCC AGC CTC CAG GCC CAG ACA GAC CGG ACT GGT Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly 50 55 60	190
GAG ATG GCC CTG CAC CTT GCA GCC CGC TAC TCA CGG GCT GAT GCT GCC Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala 65 70 75	238
AAG CGT CTC CTG GAT GCA GGT GCA GAT GCC AAT GCC CAG GAC AAC ATG Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met 80 85 90 95	286
GGC CGC TGT CCA CTC CAT GCT GCA GTG GCA GCT GAT GCC CAA GGT GTC Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val 100 105 110	334
TTC CAG ATT CTG ATT CGC AAC CGA GTA ACT GAT CTA GAT GCC AGG ATG Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met 115 120 125	382
AAT GAT GGT ACT ACA CCC CTG ATC CTG GCT GCC CGC CTG GCT GTG GAG Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu 130 135 140	430

FIG.11A

GGA ATG GTG GCA GAA CTG ATC AAC TGC CAA GCG GAT GTG AAT GCA GTG Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val 145 150 155	478
GAT GAC CAT GGA AAA TCT GCT CTT CAC TGG GCA GCT GCT GTC AAT AAT Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn 160 165 170 175	526
GTG GAG GCA ACT CTT TTG TTG TTG AAA AAT GGG GCC AAC CGA GAC ATG Val Glu Ala Thr Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met 180 185 190	574
CAG GAC AAC AAG GAA GAG ACA CCT CTG TTT CTT GCT GCC CGG GAG GGG Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly 195 200 205	622
AGC TAT GAA GCA GCC AAG ATC CTG TTA GAC CAT TTT GCC AAT CGA GAC Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp 210 215 220	670
ATC ACA GAC CAT ATG GAT CGT CTT CCC CGG GAT GTG GCT CGG GAT CGC Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg 225 230 235	718
ATG CAC CAT GAC ATT GTG CGC CTT CTG GAT GAA TAC AAT GTG ACC CCA Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro 240 245 250 255	766
AGC CCT CCA GGC ACC GTG TTG ACT TCT GCT CTC TCA CCT GTC ATC TGT Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys 260 265 270	814
GGG CCC AAC AGA TCT TTC CTC AGC CTG AAG CAC ACC CCA ATG GGC AAG Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly Lys 275 280 285	862

FIG.11B

AAG TCT AGA CGG CCC AGT GCC AAG AGT ACC ATG CCT ACT AGC CTC CCT 910
 Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser Leu Pro
 290 295 300

AAC CTT GCC AAG GAG GCA AAG GAT GCC AAG GGT AGT AGG AGG AAG AAG 958
 Asn Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys
 305 310 315

TCT CTG AGT GAG AAG GTC CAA CTG TCT GAG AGT TCA GTA ACT TTA TCC 1006
 Ser Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Ser Val Thr Leu Ser
 320 325 330 335

CCT GTT GAT TCC CTA GAA TCT CCT CAC ACG TAT GTT TCC GAC ACC ACA 1054
 Pro Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr
 340 345 350

TCC TCT CCA ATG ATT ACA TCC CCT GGG ATC TTA CAG GCC TCA CCC AAC 1102
 Ser Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn
 355 360 365

CCT ATG TTG GCC ACT GCC GCC CCT CCT GCC CCA GTC CAT GCC CAG CAT 1150
 Pro Met Leu Ala Thr Ala Ala Pro Pro Ala Pro Val His Ala Gln His
 370 375 380

GCA CTA TCT TTT TCT AAC CTT CAT GAA ATG CAG CCT TTG GCA CAT GGG 1198
 Ala Leu Ser Phe Ser Asn Leu His Glu Met Gln Pro Leu Ala His Gly
 385 390 395

GCC AGC ACT GTG CTT CCC TCA GTG AGC CAG TTG CTA TCC CAC CAC CAC 1246
 Ala Ser Thr Val Leu Pro Ser Val Ser Gln Leu Leu Ser His His His
 400 405 410 415

ATT GTG TCT CCA GGC AGT GGC AGT GCT GGA AGC TTG AGT AGG CTC CAT 1294
 Ile Val Ser Pro Gly Ser Gly Ser Ala Gly Ser Leu Ser Arg Leu His
 420 425 430

CCA GTC CCA GTC CCA GCA GAT TGG ATG AAC CGC ATG GAG GTG AAT GAG 1342
 Pro Val Pro Val Pro Ala Asp Trp Met Asn Arg Met Glu Val Asn Glu
 435 440 445

FIG.11C

ACC CAG TAC AAT GAG ATG TTT GGT ATG GTC CTG GCT CCA GCT GAG GGC	1390
Thr Gln Tyr Asn Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu Gly	
450 455 460	
ACC CAT CCT GGC ATA GCT CCC CAG AGC AGG CCA CCT GAA GGG AAG CAC	1438
Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly Lys His	
465 470 475	
ATA ACC ACC CCT CGG GAG CCC TTG CCC CCC ATT GTG ACT TTC CAG CTC	1486
Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu	
480 485 490 495	
ATC CCT AAA GGC AGT ATT GCC CAA CCA GCG GGG GCT CCC CAG CCT CAG	1534
Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln	
500 505 510	
TCC ACC TGC CCT CCA GCT GTT GCG GGC CCC CTG CCC ACC ATG TAC CAG	1582
Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu Pro Thr Met Tyr Gln	
515 520 525	
ATT CCA GAA ATG GCC CGT TTG CCC AGT GTG GCT TTC CCC ACT GCC ATG	1630
Ile Pro Glu Met Ala Arg Leu Pro Ser Val Ala Phe Pro Thr Ala Met	
530 535 540	
ATG CCC CAG CAG GAC GGG CAG GTA GCT CAG ACC ATT CTC CCA GCC TAT	1678
Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr	
545 550 555	
CAT CCT TTC CCA GCC TCT GTG GGC AAG TAC CCC ACA CCC CCT TCA CAG	1726
His Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Gln	
560 565 570 575	
CAC AGT TAT GCT TCC TCA AAT GCT GCT GAG CGA ACA CCC AGT CAC AGT	1774
His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser	
580 585 590	
GGT CAC CTC CAG GGT GAG CAT CCC TAC CTG ACA CCA TCC CCA GAG TCT	1822
Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser	
595 600 605	

FIG.11D

CCT GAC CAG TGG TCA AGT TCA TCA CCC CAC TCT GCT TCT GAC TGG TCA Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser 610 615 620	1870
GAT GTG ACC ACC AGC CCT ACC CCT GGG GGT GCT GGA GGA GGT CAG CGG Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg 625 630 635	1918
GGA CCT GGG ACA CAC ATG TCT GAG CCA CCA CAC AAC AAC ATG CAG GTT Gly Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val 640 645 650 655	1966
TAT GCG TGAGAGAGTC CACCTCCAGT GTAGAGACAT AACTGACTTT TGTAATGCT Tyr Ala	2022
GCTGAGGAAC AAATGAAGGT CATCCGGGAG AGAAATGAAG AAATCTCTGG AGCCAGCTTC	2082
TAGAGGTAGG AAAGAGAAGA TGTTCCTATT CAGATAATGC AAGAGAAGCA ATTCGTCAGT	2142
TTCACTGGGT ATCTGCAAGG CTTATTGATT ATTCTAATCT AATAAGACAA GTTTGTGGAA	2202
ATGCAAGATG AATACAAGCC TTGGGTCCAT GTTACTCTC TTCTATTTGG AGAATAAGAT	2262
GGATGCTTAT TGAAGCCCAG ACATTCTTGC AGCTTGGACT GCATTTTAAG CCCTGCAGGC	2322
TTCTGCCATA TCCATGAGAA GATTCTACAC TAGCGTCCTG TTGGGAATTA TGCCCTGGAA	2382
TTCTGCCTGA ATTGACCTAC GCATCTCCTC CTCCTTGGAC ATTCTTTTGT CTTCAATTTGG	2442
TGCTTTTGGT TTTGCACCTC TCCGTGATTG TAGCCCTACC AGCATGTTAT AGGGCAAGAC	2502
CTTTGTGCTT TTGATCATTG TGGCCCATGA AAGCAACTTT GGTCTCCTTT CCCCTCCTGT	2562
CTTCCCGGTA TCCCTTGGAG TCTCACAAGG TTTACTTTGG TATGGTTCTC AGCACAAACC	2622
TTTCAAGTAT GTTGTTCCTT TGGAAAATGG ACATACTGTA TTGTGTTCTC CTGCATATAT	2682
CATTCCTGGA GAGAGAAGGG GAGAAGAATA CTTTCTTCA ACAAATTTTG GGGGCAGGAG	2742
ATCCCTTCAA GAGGCTGCAC CTTAATTTTT CTGTCTGTG TGCAGGTCTT CATATAAACT	2802

FIG.11E

TTACCAGGAA GAAGGGTGTG AGTTTGTGT TTTCTGTGT ATGGGCCTGG TCAGTGTA	2862
TTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTTAAAA CCAGAAAAAG	2922
GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC	2982
CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT	3042
CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT	3102
AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCCTG	3162
CCATTTAGGA CTGAAC TTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT	3222
CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT	3282
TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT	3342
TTATATGTTT AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC	3402
CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT	3462
TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG	3522

FIG.11F

AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA	3582
TTGTTGAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTGGGCAATT	3642
TCTTTGACTT TCTTTTAAGG GCAGAAGCAT TTAGTTAAT TGTAGATAAA GAATAGTTTT	3702
CTTCCTCTTC TCCTTGGGCC AGTTAATAAT TGGTCCATGG CTACACTGCA ACTCCCGTCC	3762
AGTGCTGTGA TGCCCATGAC ACCTGCAAAA TAAGTTCTGC CTGGGCATTT TGTAGATATT	3822
AACAGGTGAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCCCTT CTATGGCTGC	3882
AAGTATGCAT CAGTGCTTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAAC	3942
CCTGCGTGTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCCTAT CCAAATTTAT	4002
TGAACCAACA AAAATAATTA CTTCTGCCCT GAGATAAGCA GATTAAGTTT GTTCATTCTC	4062
TGCTTTATTC TCTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATTT	4122
TATCATTCTA AATGGTGACT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA	4182
ACCTATCTGC ATGGACCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG	4242
GCGATGGCGA TGACTTTCTT CCCCTG	4268

FIG. 11G

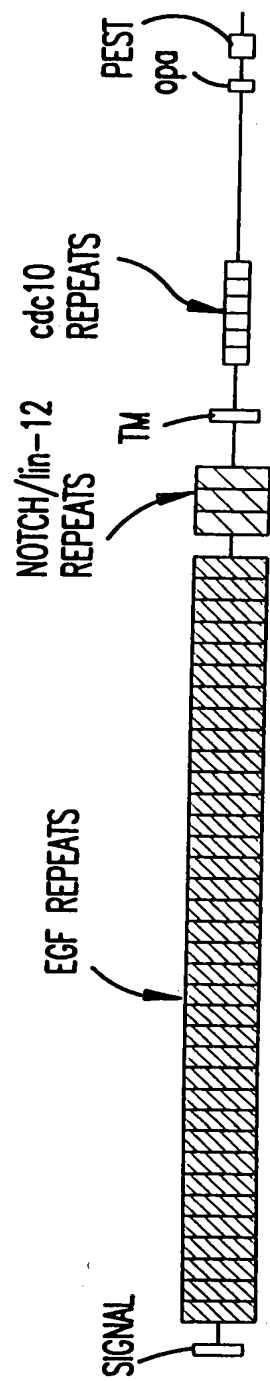


FIG.12A

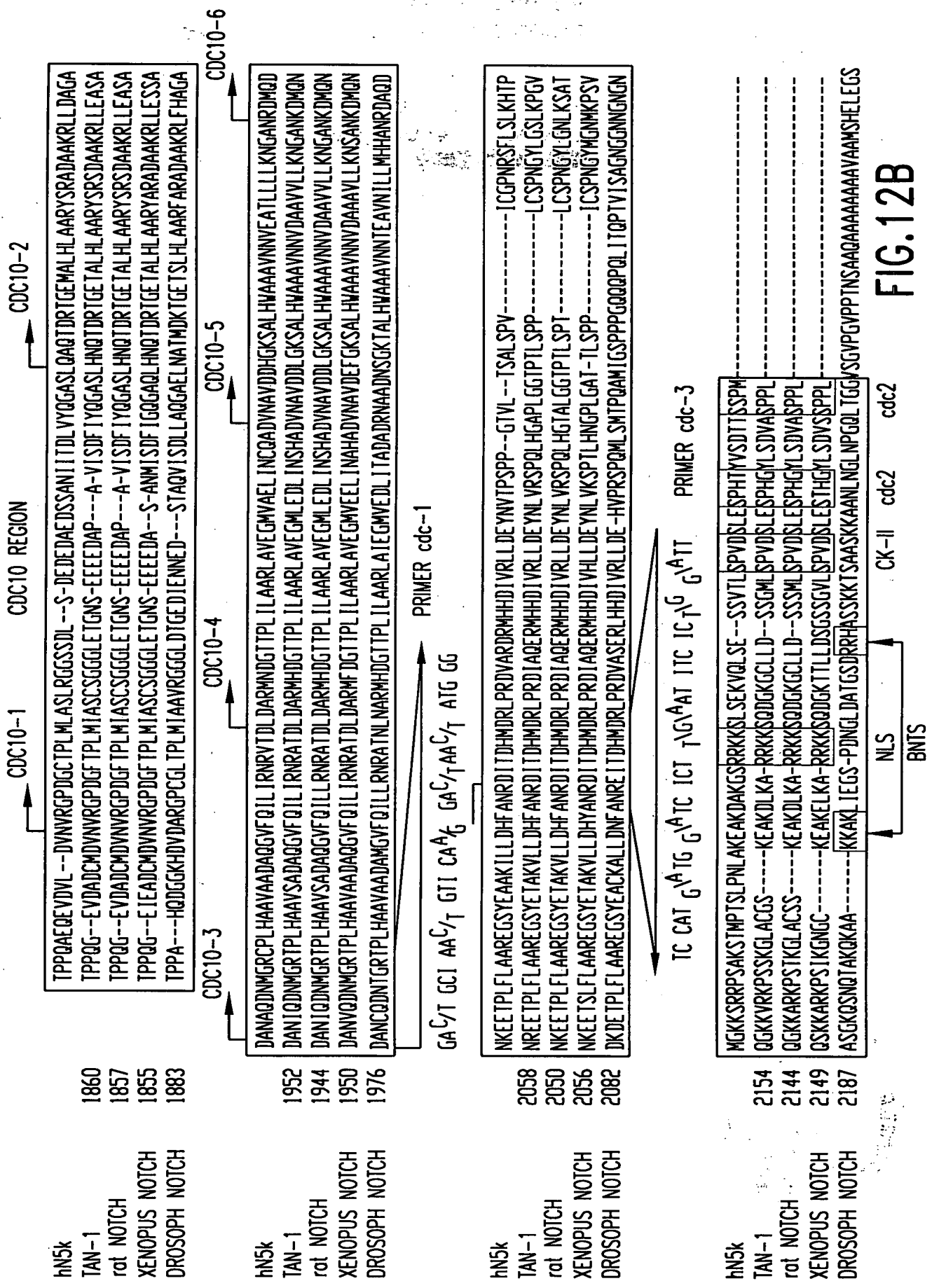


FIG.12B

Potential signal cleavage site

hum N	MP	ALRPAL	LWALLALWLC	CA	APA	HA	
TAN-1	MP	PL	LAPLLCLALL	PA	LAA	RG	
Xen N	MD	RIGLAVLLCS	LP	VLT	QG		
Dros N	MQSQRSRRRS	RAPNTWICFW	INKMHAVASL	PASLPLLLLT	LAFANLPNIV	RGTDTALVAA	

hum N	MLGKATCRCA	SGFTGEDCQY	STSHPCFVSR	PCLNGGTCHM	LSRDT-YECT	CQVGFTGKEC
Tan-1	GVADYACSCA	LGFSGPLCLT	PLDNAC-LTN	PCRNGGTCDL	LT-LTEYKCR	CPPGWSGKSC
Xen N	NAIDFICHCP	VGFTDKVCLT	PVDNAC-VNN	PCRNGGTCEL	LNSVTEYKCR	CPPGWTGDSC
Dros N	GRPGISCKCP	LGFDLSLCEI	AVPNAC-DHV	TCLNGGTCQL	KT-LEEYTC	CANGYTGERC

hum N	NLPGSYQCQC	PQGFTGQYCD	SLYVPCAPSP	CVNGGTCRQT	GDFTFECNCL	PGFEGSTCER
TAN-1	NEVGSYRCVC	RATHGPNCE	RPYVPCSPSP	CQNGGTCRPT	GDVTHECACL	PGFTQNCEE
Xen N	NEFGSYRCTC	QNRFTGRNCD	EPYVPCNPSP	CLNGGTCRQT	DDTSYDCTCL	PGFSGQNCEE
Dros N	NTHGSYQCMC	PTGYTGKDCD	TKYNPCSPSP	CQNAGICRSN	G-LSYECKCP	KGFEGKNCEE

EGF-like Repeats

QCRDGYEPCV	NEGMCVITYHN	GTGYCKPEEG	FLGEYCQHRD	PCE-KNRCQN	GGTC-VAQA	83
RCSQPGETCL	NGGKCEA-AN	GTEACVCGGA	FVGPRCQDPN	PCL-STPCKN	AGTCHVDDR	80
RCTQTAEMCL	NGGRCEMTPG	GTGVCLCGNL	YFGERCQFPN	PCTIKNQCMN	FGTCEPVLQG	90
SCTSVG-CQ	NGGTCVTQLN	GKTYCACDSH	YVG DYCEHRN	PCN-SMRCQN	GGTCQVTFRN	117

QWTDACLSPH	CANGSTCTTV	-ANQFSCKC	LTGFTGQKCE	TDVNEC-DIP	GHCQHGGTCL	199
QQADPCASNP	CANGGQCLPF	-EASYICHG	PPSFHGPTCR	QDVNECGQKP	RLCRHGGTCH	196
QQADPCASNP	CANGGKCLPF	-EIQYICKC	PPGFHGATCK	QDINEC-S-Q	NPCKNGGQCI	195
ETKNLCASSP	CRNGATCTAL	AGSSSFTCSG	PPGFTGDTCS	YDIEEC-Q-S	NPCKYGGICV	233

NIDDCPNHRC	QNGGVCVDGV	NTYNCRCPPO	WTGQFCTEDV	DECLLPNA-	CQNGGTCANR	318
NIDDCPGNNC	KNGGACVDGV	NTYNCPCPPE	WTGQYCTEDV	DECQLMPNA-	CQNGGTCHNT	315
NIDDCPSNNC	RNGGTCVDGV	NTYNQCOPPD	WTGQYCTEDV	DECQLMPNA-	CQNGGTCHNT	314
NYDDCLGHLG	QNGGTCIDGI	SDYTCRCPPN	FTGRFCQDDV	DECAQRDHPV	CQNGATCTNT	352

FIG.13A

hum N	NGGYGCVCVN	GWSGDDCSEN	IDDCAFASCT	PGSTCIDRVA	SFSCMCPEGK	AGLLCHLDDA
TAN-1	HGGYNCVCVN	GTGEDCSEN	IDDCASAACF	HGATCHDRVA	SFYCECPHGR	TGLLCHLNDA
Xen N	YGGYNCVCVN	GTGEDCSEN	IDDCANAACH	SGATCHDRVA	SFYCECPHGR	TGLLCHLDNA
Dros N	HGSYSCICVN	GWAGLDCSNN	TDDCKQAACF	YGATCIDGVG	SFYCQCTKGK	TGLLCHLDDA

hum N	AFHCECLKGY	AGPRCEMDIN	ECHSDPCQND	ATCLDKIGGF	TCLCMPGFKG	VHCELEINEC
TAN-1	SFECQCLQGY	TGPRCEIDVN	ECVSNPCQND	ATCLDQIGEF	QCMCMGPYEG	VHCEVNTDEC
Xen N	SFQCNCPPGY	AGPRCEIDVN	ECLSNPCQND	STCLDQIGEF	QCICMPGYEG	LYCETNIDEC
Dros N	SYRCNCSQGF	TGPRCETNIN	ECESHPQCNE	GSCLDDPGTF	RCVCMPGFTG	TQCEIDIDEC

hum N	ATGFTGVLCE	ENIDNCDPDP	CHHGQCQDGI	DSYTCICNPG	YMGAIQSDQI	DECYSSPCLN
TAN-1	TEGYTGTHCE	VDIDECDDP	CHYGCKDGV	ATFTCLCRPG	YTGHHCETNI	NECSSQPCRL
Xen N	TEGFTGRHCE	QDINECIPDP	CHYGTCKDGI	ATFTCLCRPG	YTGRLCDNDI	NECLSKPCLN
Dros N	PPGYTGTSCE	ININDCDSNP	CHRGKCIDDV	NSFKCLCDPG	YTGYICQKQI	NECESNPCQF

CISNPCHKGA	LCDTNPLNGQ	YICTCPQGYK	GADCTEDVDE	CAMANSNPCE	HAGKCVNTDG	438
CISNPCNEGS	NCDTNPVNGK	AICTCPSGYT	GPACSQDVDE	CSLG-ANPCE	HAGKCINTLG	434
CISNPCNEGS	NCDTNPVNGK	AICTCPPGYT	GPACNNDVDE	CSLG-ANPCE	HGGRCTNTLG	433
CTSNPCHADA	ICDTSPINGS	YACSCATGYK	GVDCEDEIDE	CDQG-SPCE	HNGICVNTPG	470

QSNPCVNNGQ	CVDKVNRFQC	LCPPGFTGPV	CQIDIDDCSS	TPCLNGAKCI	DHPNGYECQC	558
ASSPCLHNGR	CLDKINEFQC	ECPTGFTGHL	CQYDVDECAS	TPCKNGAKCL	DGPNTYTCVC	554
ASNPCLHNGK	CIDKINEFRC	DCPTGFSGNL	CQHDFDECTS	TPCKNGAKCL	DGPNSYTCQC	553
QSNPCLNDGT	CHDKINGFKC	SCALGFTGAR	CQINIDDCQS	QPCRNRGICH	DSIAGYSCEC	590

DGRCIDLUNG	YQCNCQPGTS	GVNCEINFDD	CASNPCIHG-	ICMDGINRYS	CVCSPGFTGQ	677
RGTCQDPDNA	YLCFCLKGTT	GPNCEINLDD	CASSPCDSG-	TCLDKIDGYE	CACEPGYTGS	673
GGQCTDRENG	YICTCPKGTT	GVNCEKIDD	CASNLCDNG-	KCIDKIDGYE	CTCEPGYTGK	672
DGHCQDRVGS	YYCQCQAGTS	GKNCEVNVNE	CHSNPCNNGA	TCIDGINSYK	CQCVPGFTGQ	710

FIG.13B

hum N	RCNIDIDECA	SNPCRKGATC	INGVNGFRCI	CPEGPHHPSC	YSQVNECLSN	PCI-HGNCTG
TAN-1	MCNSNIDECA	GNPCHNGGTC	EDGINGFTCR	CPEGYHDPTC	LSEVNECNSN	PCV-HGACRD
Xen N	LCNININECD	SNPCRNGGTC	KDQINGFTCV	CPDGYDHMC	LSEVNECNSN	PCI-HGACHD
Dros N	HCEKNVDECI	SSPCANNGVC	IDQVNGYKCE	CPRGFYDAHC	LSDVDECASN	PCVNEGRCED

hum N	DECASNPCLN	QGTCFDDISG	YTCHCVLPYT	GKNCQTVLAP	CSPNPCENAA	VCKESPNFES
TAN-1	NECASNPCLN	KGTCIDDVAG	YKCNCLLPYT	GATCEVVLAP	CAPSPCRNGG	ECRQSEDYES
Xen N	NECSSNPCLN	HGTCIDDVAG	YKCNMLPYT	GAICEAVLAP	CAGSPCKNGG	RCKESEDFT
Dros N	DDCVTNPCGN	GGTCIDKVN	YKCVCKVPFT	GRDCESKMDP	CASNRCNEA	KCTPSSNFLD

hum N	CLANPCQNGG	SCMDGVNTFS	CLCLPGFTGD	KCQTDNMECL	SEPCKNGGTC	SDYVNSYTCK
TAN-1	CRPNPCHNGG	SCTDGINTAF	CDCLPGFRGT	FCEEDINECA	SDPCRNGANC	TDCVDSYTCT
Xen N	CQPNPCHNGG	SCSDGINMFF	CNCPAGFRGP	KCEEDINECA	SNPCKNGANC	TDCVNSYTCT
Dros N	CASFPCQNGG	TCLDGIGDYS	CLCVDGFDGK	HCE TDINECL	SQPCQNGATC	SQYVNSYTCT

GLSGYKCLCD	AGWVGINCEV	DKNECLSNPC	QNGGTCDNLV	NGYRCTCKKG	FKGYNCQVNI	796
SLNGYKCDGD	PGWSGTNCDI	NNNECESNPC	VNGGTCKDMT	SGIVCTCREG	FSGPNCQTNI	792
GVNGYKCDCE	AGWSGSNCDI	NNNECESNPC	MNGGTCKDMT	GAYICTCKAG	FSGPNCQTNI	791
GINEFICHCP	PGYTGRCEL	DIDECSSNPC	QHGGTCYDKL	NAFSCQCMGP	YTGQKCE TNI	830

YTCLCA-PGW	QGQRTIDID	EC-ISKPCMN	HGLCHNTQGS	YMCECPPGFS	GMDCEEDIDD	914
FSCVCPTAGA	KQQTCEVDIN	EC-VLSPCRH	GASCQNTGG	YRCHCQAGYS	GRNCETDIDD	911
FSCECP-PGW	QGQTCEIDMN	EC-VNRPCRN	GATCQNTGS	YKCNCKPGYT	GRNCMDIDD	909
FSCTCK-LGY	TGRYCEDID	ECSLSSPCRN	GASCLNVPGS	YRCLCTKGYE	GRDCAINTDD	949

CQAGFDGVHC	ENNINECTES	SCFNGGTCVD	GINSFSCLCP	VGFTGSFCLH	EINECSSHPC	1034
CPAGFSGIHC	ENNTPDCTES	SCFNGGTCVD	GINSFTCLCP	PGFTGSYCQH	VVNECDSRPC	1031
CQPGFSGIHC	ESNTPDCTES	SCFNGGTCID	GINTFTCQCP	PGFTGSYCQH	DINECDSPKC	1029
CPLGFSGINC	QTNDEDCTES	SCLNGGSCID	GINGYNC SCL	AGYSGANCQY	KLNKCD SNPC	1069

FIG.13C

hum N	LNEGTCVDGL	GTYRCSCPLG	YTGKNCQTLV	NLCSPSPCKN	KGTCVQKKA	SQCLCPSGWA
TAN-1	LLGGTCQDGR	GLHRTCPQG	YTGPNQNLV	HWCDSSPCKN	GGKCWQHTQ	YRCECPSGWT
Xen N	LNGGTCQDSY	GTWKCTCPQG	YGLNCQNLV	RWCDSSPCKN	GGKCWQTNF	YRCECKSGWT
Dros N	LNGATCHEQN	NEYTCHCPSG	FTGKQCSEYV	DWCGQSPCEN	GATCSQMKHQ	FSCCKSAGWT

hum N	SNPCQHGATC	SDFIGGYRCE	CVPGYQGVNC	EYEVDECQNG	PCQNGGTCID	LVNHFKCSCP
TAN-1	PSPCQNGATC	TDYLGGYSCK	CVAGYHGVNC	SEEIDECLSH	PCQNGGTCLD	LPNTYKCS
Xen N	PNPCQNGATC	TDYLGGYSCE	CVAGYHGVNC	SEEINECLSH	PCQNGGTCID	LINTYKCS
Dros N	SQPCQNGGTC	RDLIGAYECQ	CRQGFQGNQ	ELNIDDCAPN	PCQNGGTCHD	RVMNFS

hum N	CLSNPCSSG	SLDCIQLTND	YLCVCRSAFT	GRHCETFDV	CPQMPCLNGG	TCAVASNMPD
TAN-1	CLSNPCDARG	TQNCVQRVND	FHCECRAGHT	GRRCESVING	CKGKPCKNNG	TCAVASNTAR
Xen N	CLSNPCDSRG	TQNCIQLVND	YRCECRQFT	GRRCESVVDG	CKGMPCRNGG	TCAVASNTAR
Dros N	CLSNPCSNAG	TLDCVQLVNN	YHCNCRPGHM	GRHCEHKVDF	CAQSPCQNGG	NCNI—RQS

GAYCDVPNVS	CDIAASRRGV	LVEHLCQHSG	VCINAGNTHY	CQCPLGYTGS	YCEEQLDECA	1154
GLYCDVPSVS	CEVAAQRQGV	DVARLCQHGG	LCVDAGNTHH	CRCQAGYTGS	YCEDLVDECS	1151
GVYCDVPSVS	CEVAAKQQGV	DIVHLCRNSG	MCVDTGNTHF	CRCQAGYTGS	YCEEQVDECS	1149
GKLCDVQTIS	CQDAADRKGL	SLRQLC—NNG	TCKDYGNSHV	CYCSQGYAGS	YQKEIDECQ	1188

PGTRGLLEE	NIDDCAR—	—GPHCLN	GGQCMDRIGG	YSCRCLPGFA	GERCEGDINE	1267
RGTQGVHCEI	NVDDCNPPVD	PVSRSPKCFN	NGTCVDQVGG	YSCTCPPGFV	GERCEGDVNE	1271
RGTQGVHCEI	NVDDCTPFYD	SFTLEPKCFN	NGKCIDRVGG	YNCICPPGFV	GERCEGDVNE	1269
PGTMGIICEI	NKDDCKP—	—GACHN	NGSCIDRVGG	FECVCQPGFV	GARCEGDINE	1300

GFICRCPPGF	SGARCQS—	SCGQVKCRKG	EQCVHTAS—	GPRCFCPSP—	—RDCE—	1376
GFICKCPAGF	EGATCENDAR	TCGSLRCLNG	GTCISGPR—	SPTCLCLPGF	TGPECQFPAS	1389
GFICKCPPGF	DGATCEYDSR	TCSNLRQNG	GTCISVLT—	SSKVCSEGY	TGATCQYPVI	1387
GHCICNNGF	YGKNCELSGQ	DCDSNPCRVG	—NCVVADEGF	GYRCECPRG	LGEHCEIDL	1415

FIG.13D

hum N	-GC-ASSPCQ	HGGSCHPQRQ	PPYYSCQCAP	PFSGSRCEL	-YTAPP	-S	TPP
TAN-1	SPCLGGNPCY	NQGTCEPTSE	SPFYRCLCPA	KFNGLLCHIL	DYSFGG	-GAGRD	IPPP
Xen N	SPC-ASHPCY	NGGTCQFFAE	EPFFQCFCPK	NFNGLFCHIL	DYEFPG	-GLGKNIT	TPP
Dros N	DEC-SPNPCA	QGAACEDLLG	D-YECLCPS	KWKGRCDIY	DANYPGWNGG	SGSGNDRYAA	

hum N	NN-QCDELGN	TVECLFDNFE	CQGNSTCK-	-YDKYCADHF	KDNHCNQGCN	SEECGWDGLD
TAN-1	SDGHCDQCN	SAGCLFDGFD	CQRAEGQCNP	LYDQYCKDHF	SDGHCDQGCN	SAECEWDGLD
Xen N	NDGKCDQCN	NTGCLYDGF	CQKVEVQCNP	LYDQYCKDHF	QDGHCDQGCN	NAECEWDGLD
Dros N	KNGKCNEECN	NAACHYDGH	CERKLKSCDS	LFDAYCQKHY	GDGFCDYGCN	NAECSDGLD

hum N	YYGEKSAAMK	KQ-R		MTRRSL	PGEQ	E	QEVAGSKVFL
TAN-1	YYGREEELRK	HPIKRAAEGW	AAPDALLQGV	KASLLPGGSE	GRRRRRELD	MDVRGSIVYL	
Xen N	YYGNEEELKK	HHIKRSTDY	SDAPSAI	-FSTMKESIL	LGRHRRELD	MEVRGSIVYL	
Dros N	WKDNVRVPEI	EDTDFARKNK	ILYTQQVHQ			TGIQIYL	

LNR (Notch/Lin-12 Repeats)

—A—TCL	SOYCADKARD	GVCDEACNSH	ACQWDGGDCS	LTMENPWANC	SSPLPCWDYI	1476
LIEE—ACE	LPECQEDAGN	KVCSLQCNNH	ACGWDGGDCS	LNFNDPWKNC	TQSLQCWKYF	1501
DNDD—ICE	NEQCSELADN	KVCNANCNNH	ACGWDGGDCS	LNFNDPWKNC	TQSLQCWKYF	1498
DLEQQRAMCD	KRGCTEKQGN	GICSDCNTY	ACNFDGNDCS	LGI-NPWANC	TAN-EXWNKF	1531

CAADQPEN-L	AEGTLVIVVL	MPPEQLLQDA	R-SFLRALGT	LLHTNLRIR	DSQELMVYP	1591
CAEHVPER-L	AAGTL-VVVV	LMPPEQLRNS	SFHFRLRELSR	VLHTNVVFKR	DAHGQQMIFP	1619
C-ANMPEN-L	AEGTLVLVVL	MPPERLKNNS	V-NFLRELSR	VLHTNVVFKK	DSKGEYKIYP	1615
CENKTQSPVL	AEGAMSVML	MNVEAFREIQ	A-QFLRNMSH	MLRTTVRLKK	DALGHDIIIN	1650

EIDNRQCVQD	SDHCFKNTDA	AAALLASHAI	QG—TLSYP	LVSIVSESLT	PERT-Q	LLY	1680
EIDNRQCVQA	SSQCFQSATD	VAAFLGALAS	LGSL-NIPYK	IEAVQSETVE	PPPPAQ	LHF	1737
EIDNRQCYKS	SSQCFNSATD	VAAFLGALAS	LGSLDTLSYK	IEAVKSENME	TPKPST	LYP	1730
EIDNRKCTEC	FTHAVEAAEF	LAATAAKHQL	RNDFQ-IHSV	RGIKNPGDED	NGEPPAN	VKY	1745

FIG.13E

hum N	LLAVAVVIL	FIILLGVIMA	KRKRK—HGS	LWLPEGFTLR	RDASNHKRRE	PVGQDAVGLK
TAN-1	MYVAAAFVL	LFFVCGVLL	SRKRRRQHGG	LWFPEGFKV—	SEASKKKRRE	ELGEDSVGLK
Xen N	MLSMVLPILL	IIFVFMVIV	NKKRRREHDS	FGSPTALFQK	NPA—KRNGET	PW—EDSVGLK
Dros N	VITGIILVII	ALAFFGMVL—	STQRKRAHGV	TWFPEGFRAP	AAVMSRRRRD	PHGQEMRNLN

CDC-10/Ankyrin Repeats

hum N	PIDRRPWTQQ	HLEAADIRRT	PSLALTPPQA	EQEVDVLDVN	VRGPDGCTPL	MLASLRGGSS
TAN-1	QTDHRQWTQQ	HLDAADL—RM	SAMAPTPPQG	EVDADCMDVN	VRGPDGFTPL	MIASCSGGGL
Xen N	KTDPRQWTRQ	HLDAADL—RI	SSMAPTPPQG	EIEADCMDVN	VRGPDGFTPL	MIASCSGGGL
Dros N	EADQRVWSQA	HLDVVDV—R—	AIM—TPP—A	HQDGGKHDVD	ARGPCGLTPL	MIAAVRGGGL

hum N	ANAQDNMGRG	PLHAAVAADA	QGVFQILIRN	RVTDL DARMN	DGTTPLILAA	RLAVEGMVAE
TAN-1	ANIQDNMGRT	PLHAAVSADA	QGVFQILIRN	RATDL DARMH	DGTTPLILAA	RLAVEGMLED
Xen N	ANVQDNMGRT	PLHAAVAADA	QGVFQILIRN	RATDL DARMF	DGTTPLILAA	RLAVEGMVEE
Dros N	ANCQDNTGRT	PLHAAVAADA	MGVFQILLRN	RATNLNARMH	DGTTPLILAA	RLAIEGMVED

NLSVQVSEAN	LIGTGTSEHW	VDDE—	—	—G	PQPKKKAED	EALLSE—EDD	1782
PLK—NASDGA	LMDDNQNE—W	GDED—	—	—	LETKKRFEE	PVLPD—LDD	1837
PIK—NMTDGS	FMDNQNE—W	GDEET—	—	—	LENKRFRFEE	QVILPELVDD	1831
KQVAMQSQGV	GQPGAH—W	SDDES DMPLP	KRQRSDPVSG	VGLGNNGGYA	SDHTMVSEYE		1861

DLSDDEDAAE	DSSANIITDL	VYQGASLQAQ	TORTGEMALH	LAARYSRADA	AKRLLDAGAD	1902
ETGNSEEE—E	DAPA—VISDF	IYQGASLHNQ	TORTGETALH	LAARYSRSDA	AKRLLEASAD	1954
ETGNSEEE—E	DASANMISDF	IGQGAQLHNQ	TORTGETALH	LAARYARADA	AKRLLESSAD	1949
DTGEDIENNE	DSTAQVISDL	LAQGAELNAT	MDKTGETSLH	LAARFARADA	AKRLLDAGAD	1976

LINCQADVNA	VDDHGKSALH	WAAAVNNVEA	TLLLLKNGAN	RDMQDNKEET	PLFLAAREGS	2022
LINSHADVNA	VDDLGKSALH	WAAAVNNVDA	AVLLKNGAN	KDMQNNREET	PLFLAAREGS	2074
LINAHADVNA	VDEFGKSALH	WAAAVNNVDA	AAVLLKNSAN	KDMQNNKEET	SLFLAAREGS	2069
LITADADINA	ADNSGKTALH	WAAAVNNTEA	VNILLMHAN	RDAQDDKDET	PLFLAAREGS	2096

FIG.13F

hum N	YEAAILLDH	FANRDITDHM	DRLPRDVARD	RMHHDIVRL	DEYNVTPSP	—GTVL—TS
TAN-1	YETAKVLLDH	FANRDITDHM	DRLPRDIAQE	RMHHDIVRL	DEYNLVRSPQ	LHGAPLGGP
Xen N	YETAKVLLDH	YANRDITDHM	DRLPRDIAQE	RMHHDIVHLL	DEYNLVKSPT	LHNGPLGAT—
Dros N	YEACKALLDN	FANREITDHM	DRLPRDVASE	RLHHDIVRL	DE—HVPRSPQ	MLSMTQAMI

	NLS		CK II	cdc2	cdc2	
hum N	GSRRKKSLE	KVQLSE—SS	VTLSPVDSLE	SPHTYVSDTT	SSPM	—
TAN-1	A—RRKKSQDG	KGCLLD—SS	GMLSPVDSLE	SPHGYSOVA	SPPL	—
Xen N	A—RRKKSQDG	KTTLLDSCSS	GVLSPVDSLE	STHGYSOVS	SPPL	—
Dros N	GS—PDNGLDA	TGSLRRKASS	KKTSAAASKA	ANLNGLNPGQ	LTGGVSGVPG	VPPTNSAAQA
	BNTS					

hum N	—	—	—	ITSPGILQAS	PNPML—ATA	APPAPVHAQH
TAN-1	—	—	—	LPSPF—QOS	PSVPLNHLPG	MPDTHLGIGH
Xen N	—	—	—	MTSPF—QOS	PSMPLNHLTS	MPESQLGMNH
Dros N	YEDCIKNAQS	MSLQGNGLD	MIKLDNYAYS	MGSPF—QOE	LLNGQGLGMN	GNGQRNGVGP
	CK II			cdc2		

ALSPV—	—ICGP	NRSFLSLKHT	PMGKKSRRPS	AKSTMPTSLP	NLAKEAKDAK	2127
TLSPP—	—LCSP	NGYLGSLKPG	VQKKVRKPS	SKGLACGS—	—KEAKDLK	2178
TLSPP—	—ICSP	NGYMGNMKPS	VQSKKARKPS	IKNGC—	—KEAKELK	2170
GSPPPGQQP	QLITQPTVIS	AGNGGNGNG	NASGKQSNQT	AKQKAA—	—KKAKLIE	2208

—	—	—	—	—	—	2169
—	—	—	—	—	—	2219
—	—	—	—	—	—	2213
AAAAAAVAA	MSHELEGSPV	GVGMGCNLPS	PYDTSSMYSN	AMAAPLANGN	PNTGAKQPPS	2327

ALSFSNLHEM Q—	—	—	—PLAHGASTV	LPSVSQLLSH	HHIVSPGS—	2235
LNVA—KPEM	AALGGGRLA	FETGPPRLSH	LPVAGTSTV	LGSSSGGALN	FTVGGSTSLN	2306
INMAT—KQEM	AA—GSNRMA	FDAMVPRLTH	L—NASSPNTI	MS—NGSMH	FTVGGAPTMM	2294
GVLPGGLCGM	GGLSGAGNGN	SHEQGLSPPY	SNQSPPHSVQ	SSLALSPHAY	LGSPSPAKSR	2445

FIG.13G

hum N GSAGSLRLH PVPVPADW— MNRMEVNETQ YNEMFGMVL A PAEG-THPGI APQSRPPEGK
TAN-1 GQCEWLSRLQ SGMVFNQYNP LRGSVAPGPL STQAPSLQHG -MVGPLHSSL AASALSQMMS
Xen N SQCDWLARLQ NGMVQNQYDP- IRNGIQQGN- AQQAQALQHG LMTS-LHNGL PATTLSQMMT
Dros N PSLPTSPTHI QAMRHATQKQ QFGGSNLNSL LGGANGGGGV GGGGGGGGV GQGPQNSPVS

hum N APQPQSTCPP AVAGPLPTMY QIP—EM ARL-PSVAFP TAMMPQQDGQ VAQTILPAYH
TAN-1 PPQPHLGVS AASCHLGRSF LSGEPSQADV QPLGPSSLAV HTILPQ-ESP ALPTSLPSSL
Xen N MQQQHNN-SS TTSTHINSF CSSDISQTDL QQM-SSNNI HSVMPQ-DTQ IFAASLPSNL
Dros N QQQLGGLEFG SAGLDLNG-F CGSPDSFHSG QMNPPS—I QSSMSG-SSP STNMLSPSSQ

hum N SDWSDVTTSP TPGGAGGGQR GPGTHMSEPPHNN MQVYA
TAN-1 SDWSEGVSSP PT—SMQ SQIARIPEAFK
Xen N SDWSEGISSP PT—SMQ PQRTHIPEAFK
Dros N SDWSEGVQSP AANNLYISGG HQANKGSEAIYI

—HITTPRE PLPP-IV-TF QLIPKGSIAQ PAG— 2320
—YQGLPSTRL ATQPHLVQTQ QVQPQNLQMQ QQNLQPANIQ QQQSLQPPPP 2414
—YQAMPNTRL ANQPHLMQAQ QMQQQQN— —LQLHQS 2384
LGIISPTGSD MGIMLAPPQS SKNSAIMQTI SPQQQQQQQQ QQQQQHQQQQ QQQQQQQQQQ 2565

PEST -containing Region

PFPASVGKYP TPPSQHSYAS SNAARTPSH SGHLQGEHPY LTPSPESPDQ WSSSSPHSA- 2433
VPPVTAAQFL TPPSQHSY-S S-PVENTPSH QLQVP-EGPF LTPSPESPDQ WSSSSPHSNV 2530
TQSMTTAQFL TPPSQHSY-S S-PMDNTPSH QLQVP-DHPF LTPSPESPDQ WSSSSPHSNM 2497
HNQAFYQYL TPSSQHS— —GGHTPQH LVQTL-D-SY PTPSPESPGH WSSSSPRSN- 2671

2471
2556
2523
2703

FIG.13H

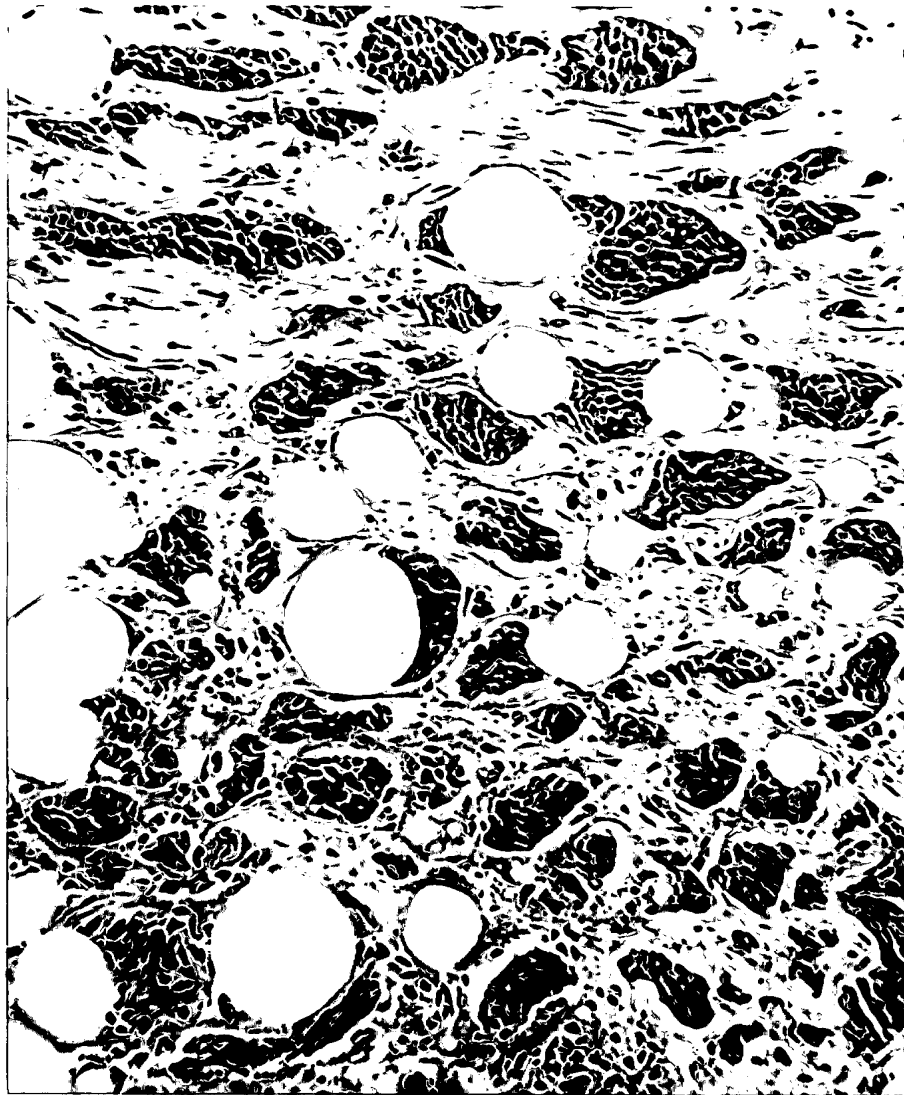


FIG.14

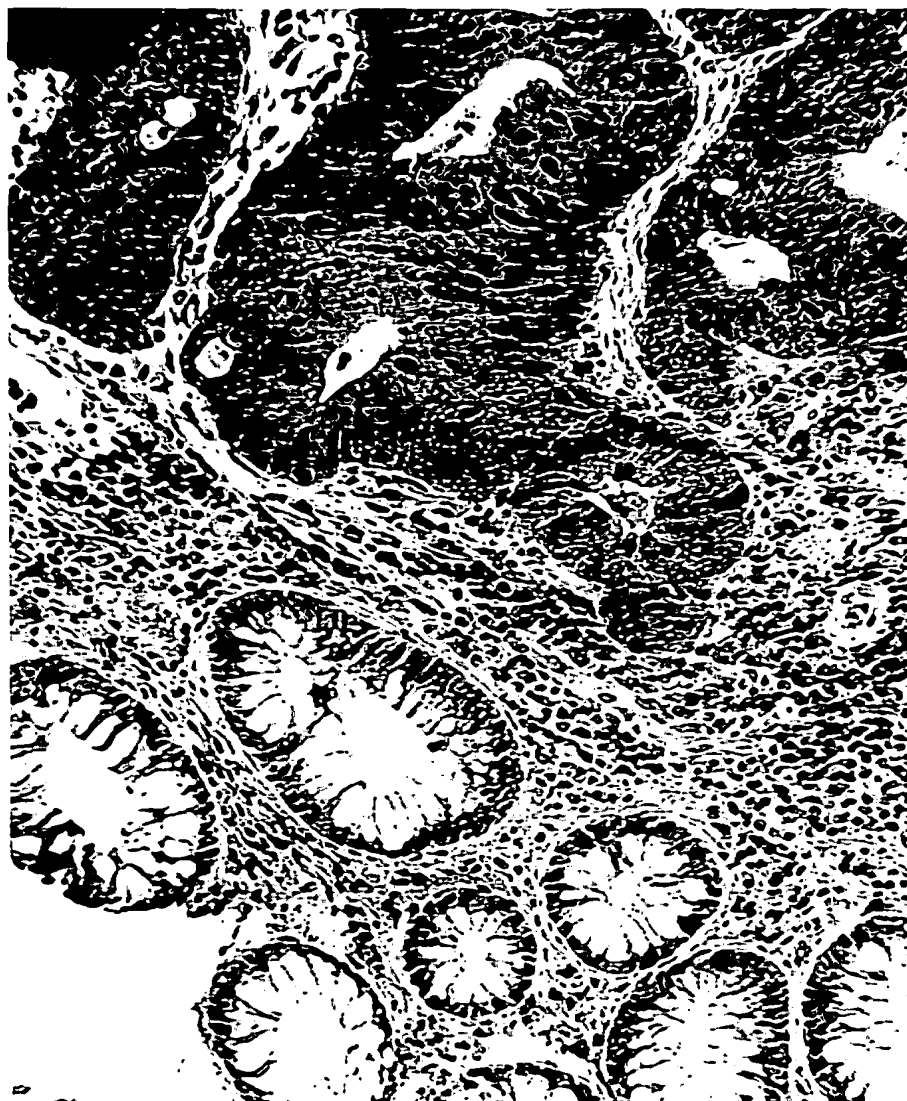


FIG.15A



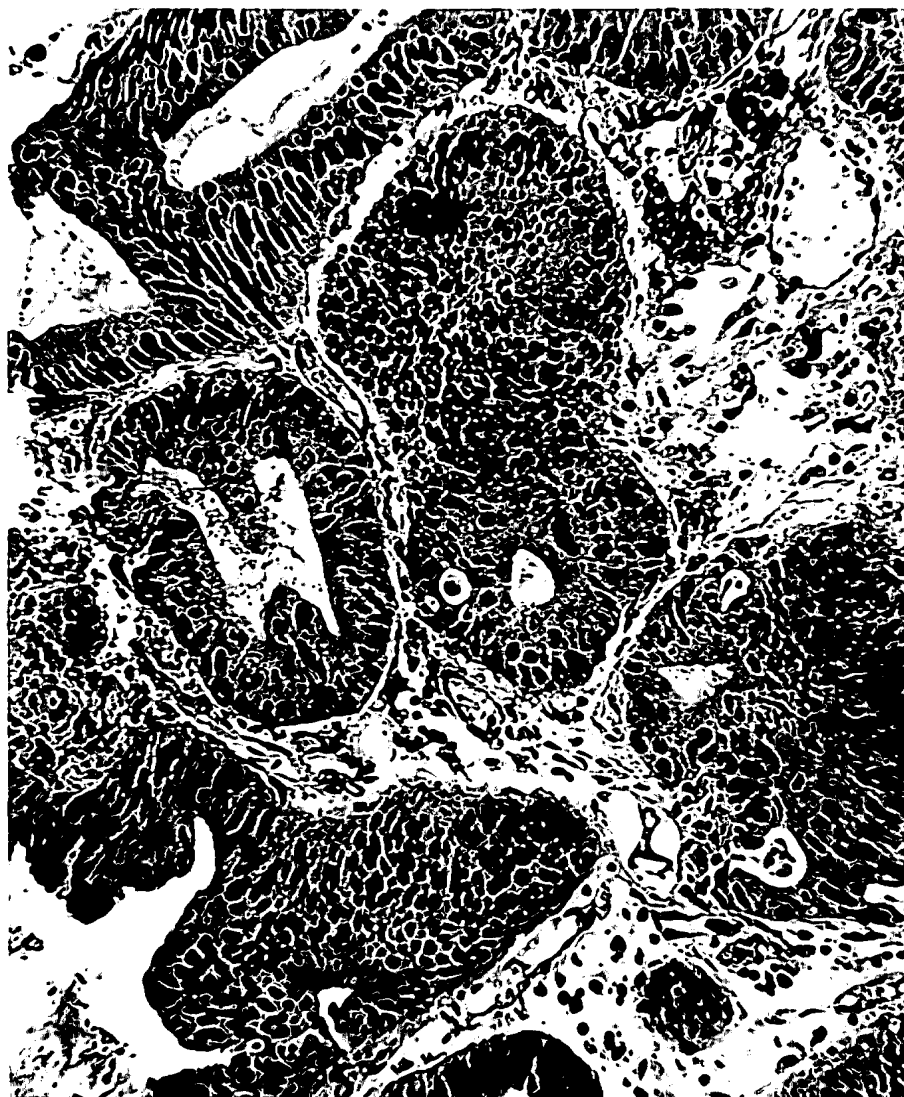


FIG.15B





FIG.16A





FIG.16B



10 20 30 40 50 60 70 80 90
 GGAATTCGGC CCGCCCTGGC CCGCGCTCTG CTGTGGGGCC TGCTGGCGCT CTGGGTGTGC TCGCGGGCCC CCGCGCATGC ATTGCACTGT
 P A L R P A L L W A L L A L W L C C A A P A H A L Q C>
 100 110 120 130 140 150 160 170 180
 CGAGATGGCT ATGAACCTGT TGTAATGAA GGAATGTGT TTACCTACCA CAATGGCACA GGATACTGCA AATGTCCAGA AGGCTTCTTG
 R D G Y E P C V N E G M C V T Y H N G T G Y C K C P E G F L>
 190 200 210 220 230 240 250 260 270
 GGGGAATATT GTCAACATCG AGACCCCTGT GAGAAGAACC GCTGCCAGAA TGGTGGGACT TGTGTGGCCC AGCCCATGCT GGGGAAAGCC
 G E Y C Q H R D P C E K N R C Q N G G T C V A Q A M L G K A>
 280 290 300 310 320 330 340 350 360
 ACGTCCGAT GTGCCTCAGG GTTACAGGA GAGGACTGCC AGTACTCAAC ATCTCATCCA TGCTTTGTGT CTGACCCCTG CCTGAATGCC
 T C R C A S G F T G E D C Q Y S T S H P C F V S R P C L N G>
 370 380 390 400 410 420 430 440 450
 GGCACATGCC ATATGCTCAG CCGGGATACC TATGAGTGCA CCTGTCAAGT CCGGTTTACA CGTAAGGAGT GCCAATGGAC GGATGCCCTGC
 G T C H M L S R D T Y E C T C Q V G F T G K E C Q W T D A C>
 460 470 480 490 500 510 520 530 540
 CTGTCTCATC CCTGTGCAAA TGGAAGTACC TGTACCACTG TGGCCAACCA GTTCTCCTGC AAATGCCTCA CAGGCTTCAC AGGGCAGAAA
 L S H P C A N G S T C T T V A N Q F S C K C L T G F T G Q K>
 550 560 570 580 590 600 610 620 630
 TGTGAGACTG ATGTCAATGA GTGTGACATT CCAGGACACT GCCAGCATGG TGGCACCTGC CTCAACCTGC CTGGTTCCCTA CCAGTCCCAG
 C E T D V N E C D I P G H C Q H G G T C L N L P G S Y Q C Q>
 640 650 660 670 680 690 700 710 720
 TGGCCTCAGG GCTTCACAGG CCAGTACTGT GACAGCCTGT ATGTGCCCTG TGCACCCTCA CCTGTGTCA ATGGAGGCAC CTGTGGGCAG
 C P Q G F T G Q Y C D S L Y V P C A P S P C V N G G T C R Q>
 730 740 750 760 770 780 790 800 810
 ACTGGTGAAT TCACTTTTGA GTGCAACTGC CTTCCAGGTT TTGAAGGGAG CACCTGTGAG AGGAATATTG ATGACTGCCC TAACCACAGG
 T G D F T F E C N C L P G F E G S T C E R N I D D C P N H R>

FIG.17A

820 830 840 850 860 870 880 890 900
 TGTGAGAATG GAGGGGTTTG TGTGGATGGG GTCAACACTT ACAACTGCCC CTGTCCCCCA CAATGGACAG GACAGTTCTG CACAGAGGAT
 C Q N G G V C V D G V N T Y N C R C P P Q W T G Q F C T E D>
 910 920 930 940 950 960 970 980 990
 GTGGATCAAT GCCTGCTGCA GCCCAATGCC TGTCAAAATG GGGGCACCTG TGCCAACCGC AATGGAGGCT ATGGCTGTGT ATGTGTCAAC
 V D E C L L Q P N A C Q N G G T C A N R N G G Y G C V C V N>
 1000 1010 1020 1030 1040 1050 1060 1070 1080
 GGCTGGAGTG GAGATGACTG CAGTGACAAC ATTGATGATT GTGCCITCGC CTCCTGTACT CCAGGCTCCA CCTGCATCCA CCGTGTGCCC
 G W S G D D C S E N I D D C A F A S C T P G S T C I D R V A>
 1090 1100 1110 1120 1130 1140 1150 1160 1170
 TCCTTCTCTT GCATGTGCCC AGAGGGGAAG GCAGGTCTCC TGTGTCATCT GGATGATGCA TGCATCAGCA ATCCTTGCCA CAAGGGGGCA
 S F S C M C P E G K A G L L C H L D D A C I S N P C H K G A>
 1180 1190 1200 1210 1220 1230 1240 1250 1260
 CTGTGTGACA CCAACCCCTT AAATGGGCAA TATATTGCA CCTGCCCACA AGGCTACAAA GGGGCTGACT GCACAGAAGA TGTGGATGAA
 L C D T N P L N G Q Y I C T C P Q G Y K G A D C T E D V D E>
 1270 1280 1290 1300 1310 1320 1330 1340 1350
 TGTGCCATGG CCAATAGCAA TCCTTGTGAG CATGCAGGAA AATGTGTGAA CACGGATGGC GCCTTCCACT GTGAGTGTCT GAAGGGTTAT
 C A M A N S N P C E H A G K C V N T D G A F H C E C L K G Y>
 1360 1370 1380 1390 1400 1410 1420 1430 1440
 GCAGGACCTC GTTGTGAGAT GGACATCAAT GAGTGGCATT CAGACCCCTG CCAGAATGAT GCTACCTGTC TGGATAAGAT TGCAGGCTTC
 A G P R C E M D I N E C H S D P C Q N D A T C L D K I G G F>
 1450 1460 1470 1480 1490 1500 1510 1520 1530
 ACATGTCTGT GCATGCCAGG TTTCAAAGGT GTGCATTGTG AATTAGAAAT AAATGAATGT CAGAGCAACC CTGTGTGAA CAATGGGCAG
 T C L C M P G F K G V H C E L E I N E C Q S N P C V N N G Q>
 1540 1550 1560 1570 1580 1590 1600 1610 1620
 TGTGTGATA AAGTCAATCG TTTCCAGTCC CTGTGTCTC CTGGTTTCAC TCGGCCAGTT TGCCAGATTG ATATTGATGA CTGTTCCAGT
 C V D K V N R F Q C L C P P G F T G P V C Q I D I D D C S S>

FIG.17B

1630 1640 1650 1660 1670 1680 1690 1700 1710
 ACTCCGTGTC TGAATGGGCG AAAGTGATC GATCACCCGA ATGGCTATGA ATGCCAGTGT GCCACAGTT TCACTGGTGT GTTGTGTCAG
 T P C L N G A K C I D H P N G Y E C Q C A T G F T G V L C E>

1720 1730 1740 1750 1760 1770 1780 1790 1800
 GAGAACATTG ACAACTGTGA CCCCATCCT TGCCACCATG GTCAGTGTC GGATGGTATT GATTCTTACA CCTGCATCTG CAATCCCGCG
 E N I D N C D P D P C H H G Q C Q D G I D S Y T C I C N P G>

1810 1820 1830 1840 1850 1860 1870 1880 1890
 TACATGGGCG CCATCTGCAG TGACCAGATT GATGAATGTT ACAGCAGCCC TTGCCTGAAC GATGGTGGCT GCATTGACCT GGTCAATGCC
 Y M G A I C S D Q I D E C Y S S P C L N D G R C I D L V N G>

1900 1910 1920 1930 1940 1950 1960 1970 1980
 TACCACTGCA ACTGCCAGCC AGGCACGTCA GCGGTTAATT GTGAAATTAA TTTTGATGAC TGTGCAAGTA ACCCTTGAT CCATGGAATC
 Y Q C N C Q P G T S G V N C E I N F D D C A S N P C I H G I>

1990 2000 2010 2020 2030 2040 2050 2060 2070
 TGTATGGATG GCATTAATCG CTACAGTTGT GTCTGCTCAC CAGGATTCAC AGGGCAGAGA TGTAACATTG ACATTGATGA GTGTGCTTCC
 C M D G I N R Y S C V C S P G F T G Q R C N I D I D E C A S>

2080 2090 2100 2110 2120 2130 2140 2150 2160
 AATCCCTGTC GCAAGGGTGC AACATGTATC AACGGTGTA ATGGTTTCCG CTGTATATGC CCGAGGGAC CCCATCACCC CAGCTGCTAC
 N P C R K G A T C I N G V N G F R C I C P E G P H H P S C Y>

2170 2180 2190 2200 2210 2220 2230 2240 2250
 TCACAGGTGA ACCAATGCCT GAGCAATCCC TGCATCCATG GAACTGTAC TGGAGGTCTC AGTGGATATA AGTGTCTCTG TGATGCAGGC
 S Q V N E C L S N P C I H G N C T G G L S G Y K C L C D A G>

2260 2270 2280 2290 2300 2310 2320 2330 2340
 TGGGTTGCCA TCAACTGTGA AGTGGACAAA AATGAATGCC TTTCCAATCC ATGCCAGAAT GGAGGAACCT GTCACAATCT GGTGAATGGA
 W V G I N C E V D K N E C L S N P C Q N G G T C D N L V N G>

2350 2360 2370 2380 2390 2400 2410 2420 2430
 TACAGGTGTA CTGCAAGAA GGCCTTTAAA GCCTATAACT GCCAGGTGAA TATTGATGAA TGTGCTCAA ATCCATGCCT GAACCAAGGA
 Y R C T C K F G F K G Y N C Q V N I D E C A S N P C L N Q G>

FIG.17C

2440	2450	2460	2470	2480	2490	2500	2510	2520
•	•	•	•	•	•	•	•	•
ACCTGCTTTG ATGACATAAG TGGCTACACT TGCCACTGTG TGCTGCCATA CACAGGCAAG AATTGTCAGA CAGTATTGGC TCCCTGTTC								
T C F D D I S G Y T C H C V L P Y T G K N C Q T V L A P C S>								
2530	2540	2550	2560	2570	2580	2590	2600	2610
•	•	•	•	•	•	•	•	•
CCAAACCCTT GTGAGAAAGC TGCTGTTTGC AAAGAGTCAC CAAATTTTGA GAGTTATACT TGCTTGTCG CTTCTGGCTG GCAAGGTCAG								
P N P C E N A A V C K E S P N F E S Y T C L C A P G W Q G Q>								
2620	2630	2640	2650	2660	2670	2680	2690	2700
•	•	•	•	•	•	•	•	•
CGGTGTACCA TTGACATTGA CGAGTGTATC TCCAAGCCCT GCATGAACCA TGGTCTCTGC CATAACACCC AGGGCAGCTA CATGTGTGAA								
R C T I D I D E C I S K P C M N H G L C H N T Q G S Y M C E>								
2710	2720	2730	2740	2750	2760	2770	2780	2790
•	•	•	•	•	•	•	•	•
TGTCCACCAG GCTTCAGTGG TATGGACTGT GAGGAGGACA TTGATGACTG CCTTGCCAAT CCTTGCCAGA ATGGAGGTTT CTGTATGGAT								
C P P G F S G M D C E E D I D D C L A N P C Q N G G S C M D>								
2800	2810	2820	2830	2840	2850	2860	2870	2880
•	•	•	•	•	•	•	•	•
GGAGTGAATA CTTTCTCCTG CCTCTGCCCT CCGGGTTTCA CTGGGGATAA GTGCCAGACA GACATGAATG AGTGTCAGAG TGAACCTGT								
G V N T F S C L C L P G F T G D K C Q T D M N E C L S E P C>								
2890	2900	2910	2920	2930	2940	2950	2960	2970
•	•	•	•	•	•	•	•	•
AAGAATGGAG GGACCTGCTC TGAAGTCTC AACAGTTACA CTGGAAGTG CCAGGCAGGA TTTGATGGAG TCCATTGTGA GAACAACATC								
K N G G T C S D Y V N S Y T C K C Q A G F D G V H C E N N I>								
2980	2990	3000	3010	3020	3030	3040	3050	3060
•	•	•	•	•	•	•	•	•
AATGAGTCCA CTGAGAGCTC CTGTTTCAAT GGTGGCACAT GTGTGATCG GATTAAGTCC TTCTCTTGCT TGTGCCCTGT GGGTTTCACT								
N E C T E S S C F N G G T C V D G I N S F S C L C P V G F T>								
3070	3080	3090	3100	3110	3120	3130	3140	3150
•	•	•	•	•	•	•	•	•
GGATCCTTCT GCCTCCATGA GATCAATGAA TGCAGCTCTC ATCCATGCCT GAATGACGGA ACGTGTGTTG ATGGCCTGGG TACCTACCGC								
G S F C L H E I N E C S S H P C L N E G T C V D G L G T Y R>								
3160	3170	3180	3190	3200	3210	3220	3230	3240
•	•	•	•	•	•	•	•	•
TGCAGCTGCC CCCTGGGCTA CACTGGGAAA AACTGTCAGA CCCTGGTGAA TCTCTGCAGT CCGTCTCCAT GTAAAAACAA AGGTAAGTGT								
C S C P L G Y T G K N C Q T L V N L C S R S P C K N K G T C>								

FIG.17D

3250 3260 3270 3280 3290 3300 3310 3320 3330
 GTTCAGAAA AAGCAGATC CCAGTGCCTA TGTCATCTG GATGGGCTGG TGCCTATTGT GACGTGCCCA ATGCTCTTGG TGACATAGCA
 V Q K K A E S Q C L C P S G W A G A Y C D V P N V S C D I A>

3340 3350 3360 3370 3380 3390 3400 3410 3420
 GCCTCCAGGA GAGGTGTGCT TGTGAACAC TTGTGCCAGC ACTCAGGTCT CTGCATCAAT GCTGGCAACA CCGATTACTG TCAGTGCCCC
 A S R R G V L V E H L C Q H S G V C I N A G N T H Y C Q C P>

3430 3440 3450 3460 3470 3480 3490 3500 3510
 CTGGGCTATA CTGGGAGCTA CTGTGAGGAG CAACTCGATG AGTGTGCGTC CAACCCCTGC CAGCACGGGG CAACATGCAG TGACTTCATT
 L G Y T G S Y C E E Q L D E C A S N P C Q H G A T C S D F I>

3520 3530 3540 3550 3560 3570 3580 3590 3600
 GGTGGATACA GATCCGAGTG TGTCCCAGGC TATCAGGGTG TCAACTGTGA GTATGAAGTG GATGAGTGCC AGAATCAGCC CTGCCAGAAT
 G G Y R C E C V P G Y Q G V N C E Y E V D E C Q N Q P C Q N>

3610 3620 3630 3640 3650 3660 3670 3680 3690
 GGAGGCACCT GTATTGACCT TGTGAACCAT TTCAAGTGCT CTTGCCCACC AGGCACTCGG GGCCTACTCT GTGAAGAGAA CATTGATGAC
 G G T C I D L V N H F K C S C P P G T R G L L C E E N I D D>

3700 3710 3720 3730 3740 3750 3760 3770 3780
 TGTGCCCCGG GTCCCCATTG CCTTAATGCT GGTCACTGCA TGGATAGGAT TGGAGGCTAC AGTTGTGCGT GCTTGCCCTGG CTTTGCTCGG
 C A R G P H C L N G G Q C M D R I G G Y S C R C L P G F A G>

3790 3800 3810 3820 3830 3840 3850 3860 3870
 GAGCGTTGTG AGGGAGACAT CAACGAGTGC CTCTCCAACC CCTGCAGCTC TGAGGGCAGC CTGGACTGTA TACAGCTCAC CAATGACTAC
 E R C E G D I N E C L S N P C S S E G S L D C I Q L T N D Y>

3880 3890 3900 3910 3920 3930 3940 3950 3960
 CTGTGTGTTT GCGTAGTGC CTTTACTGGC CGGCACTGTG AAACCTTGTG CGATGTGTGT CCCCAGATGC CCTGCCTGAA TGGAGGCACT
 L C V C R S A F T G R H C E T F V D V C P Q M P C L N G G T>

3970 3980 3990 4000 4010 4020 4030 4040 4050
 TGTGCTGTGG CCAGTAACAT GCCTGATGCT TTCATTGCC GTTGTCCCC GGGATTTTCC GGGCAAGGT GCCAGAGCAG CTGTGGACAA
 C A V A S N M P D G F I C R C P P G F S G A R C Q S S C G Q>

FIG.17E

4060 4070 4080 4090 4100 4110 4120 4130 4140
 GTGAAATGTA GGAAGCGGGA GCAGTGTGTG CACACCGCCT CTGGACCCCG CTGCTTCTGC CCCAGTCCCC GGGACTCCGA GTCAGGCTGT
 V K C R K G E Q C V H T A S G P R C F C P S P R D C E S G C>

4150 4160 4170 4180 4190 4200 4210 4220 4230
 GCCAGTAGCC CCTGCCAGCA CGGGGGCAGC TGCCACCCCTC AGCGCCAGCC TCCTTATTAC TCCTGCCAGT GTGCCCCACC ATTCTCGGCT
 A S S P C Q H G G S C H P Q R Q P P Y Y S C Q C A P P F S G>

4240 4250 4260 4270 4280 4290 4300 4310 4320
 AGCCGCTGTG AACTCTACAC GGCACCCCCC AGCACCCCTC CTGCCACCTG TCTGAGCCAG TATTGTCCCG ACAAGCTCG GGATGGCGTC
 S R C E L Y T A P P S T P P A T C L S Q Y C A D K A R D G V>

4330 4340 4350 4360 4370 4380 4390 4400 4410
 TGTGATGAGG CCTGCAACAG CCATGCCTGC CAGTGGGATG GGGGTGACTG TTCTCTCACC ATGGAGAACC CCTGGGCCAA CTGCTCCTCC
 C D E A C N S H A C Q W D G G D C S L T M E N P W A N C S S>

4420 4430 4440 4450 4460 4470 4480 4490 4500
 CCACTTCCCT GCTGGGATTA TATCAACAAC CAGTGTGATG AGCTGTGCAA CACGGTCGAG TGCCTGTTTG ACAACTTTGA ATGCCAGGGG
 P L P C W D Y I N N Q C D E L C N T V E C L F D N F E C Q G>

4510 4520 4530 4540 4550 4560 4570 4580 4590
 AACAGCAAGA CATGCAAGTA TGACAAATAC TGTGCAGACC ACTTCAAAGA CAACCACTGT AACCAGGGCT GCAACAGTGA GGAGTGTGCT
 N S K T C K Y D K Y C A D H F K D N H C N Q G C N S E E C G>

4600 4610 4620 4630 4640 4650 4660 4670 4680
 TGGGATGGGC TGGACTGTGC TGCTGACCAA CCTGAGAACC TGGCAGAAGG TACCCTGGTT ATTGTGCTAT TGATGCCACC TGAACAACCTG
 W D G L D C A A D Q P E N L A E G T L V I V V L M P P E Q L>

4690 4700 4710 4720 4730 4740 4750 4760 4770
 CTCCAGGATG CTGCGAGCTT CTTGGGGGCA CTGGGTACCC TGCTCCACAC CAACCTGGCC ATTAAGCGGC ACTCCCAGGG GGAACCTCATG
 L Q D A R S F L R A L G T L L H T N L R I K R D S Q G E L M>

4780 4790 4800 4810 4820 4830 4840 4850 4860
 GTGTACCCCT ATTATGGTGA GAAGTCAGCT GCTATGAAGA AACAGAGGAT GACACGCAGA TCCCTTCCTG GTGAACAAGA ACAGGAGGTC
 V Y P Y Y G E K S A A M K K Q R M T R R S L P G E Q E Q E V>

FIG.17F

4870 4880 4890 4900 4910 4920 4930 4940 4950
 GCTGGCTCTA AAGTCTTCT GGAAATTGAC AACCGCCAGT GTGTCAAGA CTCAGACCAC TGCTCAAGA ACACGGATGC AGCAGCAGCT
 A G S K V F L E I D N R Q C V Q D S D H C F K N T D A A A A>
 4960 4970 4980 4990 5000 5010 5020 5030 5040
 CTCCTGGCT CTCACGCCAT ACAGGGGACC CTGTCATACC CTCTGTGTC TGTGTCAGT GAATCCCTGA CTCCAGAAGC CACTCAGCTC
 L L A S H A I Q G T L S Y P L V S V V S E S L T P E R T Q L>
 5050 5060 5070 5080 5090 5100 5110 5120 5130
 CICTATCTCC TTGCTGTTC TGTGTCATC ATTCTGTTA TTATTCTGCT GCGCGTAATC ATGGCAAAAC GAAAGCGTAA GCATGGCTCT
 L Y L L A V A V V I I L F I I L L G V I M A K R K R K H G S>
 5140 5150 5160 5170 5180 5190 5200 5210 5220
 CTCTGGCTGC CTGAAGGTTT CACTCTTCG CGAGATGCAA GCAATCACA GCGTCGTGAG CCAGTGGGAC AGGATGCTGT GCGGCTGAAA
 L W L P E G F T L R R D A S N H K R R E P V G Q D A V G L K>
 5230 5240 5250 5260 5270 5280 5290 5300 5310
 AATCTCTCAG TGCAAGTCTC AGAAGCTAAC CTAATTGCTA CTGGAACAAG TGAACACTGC CTCGATGATC AACGGCCCCA GCCAAAGAAA
 N L S V Q V S E A N L I G T G T S E H W V D D E G P Q P K K>
 5320 5330 5340 5350 5360 5370 5380 5390 5400
 GTAAAGGCTG AAGATGAGGC CTTACTCTCA GAAGAAGATG ACCCATTTGA TCGACGGCCA TGGACACAGC AGCACCTTGA AGCTGCAGAC
 V K A E D E A L L S E E D D P I D R R P W T Q Q H L E A A D>
 5410 5420 5430 5440 5450 5460 5470 5480 5490
 ATCCGTAGGA CACCATCGCT GGCTCTCACC CCTCCTCAGG CAGAGCAGGA GGTGGATGTG TTAGATGTGA ATGTCCGTGG CCCAGATGGC
 I R R T P S L A L T P P Q A E Q E V D V L D V N V R G P D G>
 5500 5510 5520 5530 5540 5550 5560 5570 5580
 TGCACCCCAT TGATGTTGGC TTCTCTCGA GGAGGCAGCT CAGATTGAG TGATGAAGAT GAAGATGCAG AGGACTCTTC TGCTAACATC
 C T P L M L A S L R G G S S D L S D E D E D A E D S S A N I>
 5590 5600 5610 5620 5630 5640 5650 5660 5670
 ATCACAGACT TGCTTACCA GGGTCCGAGC CTCCAGGCCC AGACAGACCG GACTGGTGAG ATGGCCCTGC ACCTTGACAG CCGCTACTCA
 I T D L V Y Q G A S L Q A Q T D R T G E M A L H L A A R Y S>

FIG.17G

5680 5690 5700 5710 5720 5730 5740 5750 5760
 CCGGCTGATG CTGCCAAGCG TCTCCTGGAT GCAGGTGCAG ATGCCAATGC CCAGGACAAC ATGGGCGGCT GTCCACTCCA TGCTGCAGTG
 R A D A A K R L L D A G A D A N A Q D N M G R C P L H A A V>

5770 5780 5790 5800 5810 5820 5830 5840 5850
 GCAGCTGATG CCCAAGGTGT CTTCCAGATT CTGATTCCGA ACCGAGTAAC TGATCTAGAT GCCAGGATGA ATGATGGTAC TACACCCCTG
 A A D A Q G V F Q I L I R N R V T D L D A R M N D G T T P L>

5860 5870 5880 5890 5900 5910 5920 5930 5940
 ATCCTGGCTG CCCGCTGGC TGTGGAGGGA ATGGTGGCAG AACTGATCAA CTCCAAGCGG GATGTGAATC CAGTGGATGA CCATGGA AAA
 I L A A R L A V E G M V A E L I N C Q A D V N A V D D H G K>

5950 5960 5970 5980 5990 6000 6010 6020 6030
 TCTGCTCTTC ACTGGGCAGC TGCTGTCAAT AATGTGGAGG CAACTCTTTT GTTGTGAAA AATGGGGCCA ACCGAGACAT GCAGGACAAC
 S A L H W A A A V N N V E A T L L L L K N G A N R D M Q D N>

6040 6050 6060 6070 6080 6090 6100 6110 6120
 AAGGAAGAGA CACCTCTGTT TCTTGCTGCC CCGGAGGGGA GCTATGAAGC AGCCAAGATC CTGTTAGACC ATTTTGCCAA TCGAGACATC
 K E E T P L F L A A R E G S Y E A A K I L L D H F A N R D I>

6130 6140 6150 6160 6170 6180 6190 6200 6210
 ACAGACCATA TGGATCGTCT TCCCCGGGAT GTGGCTCGGG ATCGCATGCA CCATGACATT GTGGCGCTTC TGGATGAATA CAATGTGACC
 T D H M D R L P R D V A R D R M H H D I V R L L D E Y N V T>

6220 6230 6240 6250 6260 6270 6280 6290 6300
 CCAAGCCCTC CAGGCACCGT GTTGACTTCT GCTCTCTCAC CTGTCATCTG TGGGCCCAAC AGATCTTTCC TCAGCCTGAA GCACACCCCA
 P S P P G T V L T S A L S P V I C G P N R S F L S L K H T P>

6310 6320 6340 6350 6360 6370 6380 6390 6400
 ATGGCAAGA AGTCTAGACG GCCCAGTCCC AAGAGTACCA TGCCTACTAG CCTCCCTAAC CTTGCCAAGG AGGCAAAGGA TGCCAAGGCT
 M G K K S R R P S A K S T M P T S L P N L A K E A K D A K G>

6400 6410 6420 6430 6440 6450 6460 6470 6480
 AGTAGGAGGA AGAAGTCTCT GAGTGAGAAG GTCCAAGTGT CTGAGAGTTC AGTAACTTTA TCCCCTGTTG ATTCCTAGA ATCTCCTCAC
 S R R K K S L S E K V Q L S E S S V T L S P V D S L E S P H>

FIG.17H

6490 6500 6510 6520 6530 6540 6550 6560 6570
 ACGTATGTTT CCGACACCAC ATCCTCTCCA ATGATTACAT CCCCTGGGAT CTACAGGCC TCACCAACC CTATGTTGGC CACTGCCGCC
 T Y V S D T T S S P M I T S P G I L Q A S P N P M L A T A A>

6580 6590 6600 6610 6620 6630 6640 6650 6660
 CCTCCTGCCC CAGTCCATGC CCAGCATGCA CTATCTTTT CTAACTTCA TGAATGCAG CCTTTGGCAC ATGGGGCCAG CACTGTGCTT
 P P A P V H A Q H A L S F S N L H E M Q P L A H G A S T V L>

6670 6680 6690 6700 6710 6720 6730 6740 6750
 CCCTCAGTGA GCCAGTTGCT ATCCACCAC CACATTGTGT CTCCAGGCAG TGCAGTGCT GGAAGCTTGA GTAGGCTCCA TCCAGTCCCA
 P S V S Q L L S H H H I V S P G S G S A G S L S R L H P V P>

6760 6770 6780 6790 6800 6810 6820 6830 6840
 GTCCAGCAG ATTGGATGAA CCGCATGAG GTGAATGACA CCCAGTACAA TGAGATGTTT GGTATGGTCC TGGCTCCAGC TGAGGGCACC
 V P A D W M N R M E V N E T Q Y N E M F G M V L A P A E G T>

6850 6860 6870 6880 6890 6900 6910 6920 6930
 CATCCTGGCA TAGCTCCCCA GAGCAGGCCA CCTGAAGGGA AGCACATAAC CACCCCTCGG GAGCCCTTGC CCCCCATTGT GACTTTCAG
 H P G I A P Q S R P P E G K H I T T P R E P L P P I V T F Q>

6940 6950 6960 6970 6980 6990 7000 7010 7020
 CTCATCCCTA AAGGCAGTAT TGCCCAACCA GCGGGGGCTC CCCAGCCTCA GTCCACCTGC CCTCCAGCTG TTGCGGGCCC CCTGCCACC
 L I P K G S I A Q P A G A P Q P Q S T C P P A V A G P L P T>

7030 7040 7050 7060 7070 7080 7090 7100 7110
 ATGTACCAGA TTCCAGAAAT GGCCCGTTTG CCCAGTGTGG CTTTCCCAC TGCCATGATG CCCCAGCAGG ACGGCAGGT AGCTCAGACC
 M Y Q I P E M A R L P S V A F P T A M M P Q Q D G Q V A Q T>

7120 7130 7140 7150 7160 7170 7180 7190 7200
 ATTCTCCCAG CCTATCATCC TTTCCAGCC TCTGTGGGCA AGTACCCAC ACCCCCTTCA CAGCACAGTT ATGCTTCTC AAATGCTGCT
 I L P A Y H P F P A S V G K Y P T P P S Q H S Y A S S N A A>

7210 7220 7230 7240 7250 7260 7270 7280 7290
 GAGCGAACAC CCAGTCACAG TGGTCACCTC CAGGGTGAGC ATCCCTACCT GACACCATCC CCAGAGTCTC CTGACCACTG GTCAAGTTCA
 E R T P S H S G H L Q G E H P Y L T P S P E S P D Q W S S S>

FIG.171

7300	7310	7320	7330	7340	7350	7360	7370	7380
•	•	•	•	•	•	•	•	•
TCACCCACT	CTGCTTCTGA	CTGGTCAGAT	GTGACCACCA	GCCCTACCCC	TGGGGGTGCT	GGAGGAGGTC	AGCGGGGACC	TGGGACACAC
S P H	S A S D	W S D	V T T	S P T P	G G A	G G G	Q R G P	G T H>

7390	7400	7410	7420	7430	7440	7450	7460	7470
•	•	•	•	•	•	•	•	•
ATGCTGAGC	CACCACACAA	CAACATCCAG	GTTTATGCGT	GAGAGAGTCC	ACCTCCAGTG	TAGAGACATA	ACTGACTTTT	GTAATGCTG
M S E	P P H N	N M Q	V Y A>					

7480	7490	7500	7510	7520	7530	7540	7550	7560
•	•	•	•	•	•	•	•	•
CTGAGGAACA	AATGAAGGTC	ATCCGGGAGA	GAATGAAGA	AATCTCTGGA	GCCAGCTTCT	AGAGGTAGGA	AAGAGAAGAT	GTTCTTATTC

7570	7580	7590	7600	7610	7620	7630	7640	7650
•	•	•	•	•	•	•	•	•
AGATAATGCA	ACAGAAGCAA	TTCGTCAGTT	TCACTGGGTA	TCTGCAAGCC	TTATTGATTA	TTCTAATCTA	ATAAGACAAG	TTTGTCGAAA

7660	7670	7680	7690	7700	7710	7720	7730	7740
•	•	•	•	•	•	•	•	•
TGCAAGATGA	ATACAAGCCT	TGGGTCCATG	TTACTCTCT	TCTATTGGA	GAATAAGATG	GATGCTTATT	GAAGCCCAGA	CATTCTTGCA

7750	7760	7770	7780	7790	7800	7810	7820	7830
•	•	•	•	•	•	•	•	•
GCTTGGACTG	CATTTTAAGC	CCTGCAGGCT	TCTGCCATAT	CCATGAGAAG	ATTCTACACT	AGCGTCTGT	TGGGAATTAT	CCCCTGGAAT

7840	7850	7860	7870	7880	7890	7900	7910	7920
•	•	•	•	•	•	•	•	•
TCTGCCCTGAA	TGACCTACG	CATCTCCTCC	TCCTTGACA	TTCTTTTGTC	TTCAATTGGT	GCITTTGGTT	TTCACCTCT	CCGTGATTGT

7930	7940	7950	7960	7970	7980	7990	8000	8010
•	•	•	•	•	•	•	•	•
AGCCCTACCA	GCATGTTATA	GGCCAAGACC	TTTGTCITTT	TGATCATTCT	GGCCCATGAA	AGCAACTTTG	GTCTCCTTTC	CCCTCCTGTC

8020	8030	8040	8050	8060	8070	8080	8090	8100
•	•	•	•	•	•	•	•	•
TTCCCGGTAT	CCCTTGAGT	CTCACAAGGT	TTACTTTGGT	ATGGTTCTCA	GCACAAACCT	TTCAAGTATG	TIGTTTCTTT	GGAAAATGGA

8110	8120	8130	8140	8150	8160	8170	8180	8190
•	•	•	•	•	•	•	•	•
CATACTGTAT	TGTGTTCTCC	TGCATATATC	ATTCTCGAG	AGAGAAGGGG	AGAAGAATAC	TTTTCTTCAA	CAAATTTTGG	GGCCAGGAGA

8200	8210	8220	8230	8240	8250	8260	8270	8280
•	•	•	•	•	•	•	•	•
TCCCTTCAAG	AGGCTGCACC	TTAATTTTTC	TTGTCTGTGT	GCAGGTCTTC	ATATAAACTT	TACCAGGAAG	AAGCGTGTGA	GTTTGTGT

FIG.17J

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8290 8300 8310 8320 8330 8340 8350 8360 8370
 TTTCTGTGTA TGGCCCTGGT CAGTGTAAG TTTTATCCTT GATAGTCTAG TTA CTATGAC CCTCCCCACT TTTTAAAC CAGAAAAAGG
 8380 8390 8400 8410 8420 8430 8440 8450 8460
 TTTGGAATGT TCGAATGACC AAGAGACAAG TTA ACTGTG CAAGAGCCAG TTACCCACCC ACAGGTCCCC CTA CTTCCTG CCAAGCATT
 8470 8480 8490 8500 8510 8520 8530 8540 8550
 CATTGACTGC CTGTATGAA CACATTTGTC CCAGATCTGA GCATTCTAGG CCTGTTTCAC TCACTCACCC AGCATATGAA ACTAGTCTTA
 8560 8570 8580 8590 8600 8610 8620 8630 8640
 ACTGTTGACC CTTTCCTTC ATATCCACAG AAGACACTGT CTCAAATGTT GTACCCCTGC CATTTAGGAC TGAACITTC TTAGCCCAAG
 8650 8660 8670 8680 8690 8700 8710 8720 8730
 GGACCCAGTG ACGTTGCT TCCGTTGTC AGATGATCAG TCTCTACTGA TTATCTGCT GCTTAAAGGC CTGCTACCA ATCTTCTTT
 8740 8750 8760 8770 8780 8790 8800 8810 8820
 CACACCGTGT GGTCCGTGTT ACTGGTATAC CCACTATGTT CTCCTGAAG ACATGGACTT TATATGTTCA AGTCCAGGAA TTGGAAGTT
 8830 8840 8850 8860 8870 8880 8890 8900 8910
 GGACTTGTTT TCTATGATCC AAAACAGCCC TATAAGAAGG TTGAAAAGG AGAACTATA TAGCAGCCTT TGCTATTTTC TGCTACCATT
 8920 8930 8940 8950 8960 8970 8980 8990 9000
 TCTTTTCTC TGAAGCGCC ATGACATTCC CTTTGGCAAC TAACGTAGAA ACTCAACAGA ACATTTTCTT TTCCTAGAGT CACCTTTTAG
 9010 9020 9030 9040 9050 9060 9070 9080 9090
 ATGATAATGC ACAACTATAG ACTTGCTCAT TGTTGAGACT GATTGCCCT CACCTGAATC CACTCTCTGT ATTCATGCTC TTGGCAATT
 9100 9110 9120 9130 9140 9150 9160 9170 9180
 CTTTGACTTT CTTTAAAGG CAGAAGCATT TTAGTTAATT GTAGATAAAG AATAGTTTC TTCTCTTCT CCTTGGGCCA GTTAATAATT
 9190 9200 9210 9220 9230 9240 9250 9260 9270
 GGTCCATGGC TAACTGCAA CTTCCGTCCA GTGCTGTGAT GCCCATGACA CCTGCAAAAT AAGTTCTGCC TGGGCATTTT GTAGATATTA

FIG.17K

9280	9290	9300	9310	9320	9330	9340	9350	9360
•	•	•	•	•	•	•	•	•
ACAGGTGAAT	TCCCGACTCT	TTTGGTTTGA	ATGACAGTTC	TCATTCCCTC	TATGGCTGCA	AGTATGCATC	AGTGCTTCCC	ACTTACCTGA
9370	9380	9390	9400	9410	9420	9430	9440	9450
•	•	•	•	•	•	•	•	•
TTTGTCTGTC	GGTGGCCCCA	TATGGAAACC	CTGGCTGTCT	GTGGGCATAA	TAGTTTACAA	ATGGTTTTTT	CAGTCCTATC	CAAATTTATT
9460	9470	9480	9490	9500	9510	9520	9530	9540
•	•	•	•	•	•	•	•	•
GAACCAACAA	AAATAATTAC	TTCTGCCCTG	AGATAAGCAG	ATTAAGTTTG	TTCATTCTCT	GCTTTATTCT	CTCCATGTGG	CAACATTCTG
9550	9560	9570	9580	9590	9600	9610	9620	9630
•	•	•	•	•	•	•	•	•
TCAGCCTCTT	TCATAGTGTG	CAAACATTTT	ATCATTCTAA	ATGGTGACTC	TCTGCCCTTG	GACCCATTTA	TTATTCACAG	ATGGGGAGAA
9640	9650	9660	9670	9680	9690	9700	9710	9720
•	•	•	•	•	•	•	•	•
CCTATCTGCA	TGGACCCTCA	CCATCCTCTG	TGCAGCACAC	ACAGTGCAGG	GAGCCAGTGG	CGATGGCGAT	GACTTTCTTC	CCCTGGGAAT

TCC

FIG.17L